

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 09:13:46 ; Search time 4994.97 Seconds
(without alignments)
1952.395 Million cell updates/sec

Title: US-09-214-124-1

Perfect score: 940

Sequence: 1 aaugugaggagcucccg.....ccucuccgcccgauggg 940

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 5187315402 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_ba2.*
3: gb_om.*
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5: gb_pat.*
6: gb_ph.*
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24: em_ph.*
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81: gb_v11.*
82: gb_v12.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	940	100.0	940 5	A83548	A83548 Sequence 1
2	825.2	87.8	4292 82	AF006065	AF006065 Fowlpox v
3	578	61.5	578 5	A83549	A83549 Sequence 2
4	529.8	56.4	543 81	S70398	S70398 (LTR, U3, R
5	512.4	54.5	583 81	S79845	S79845 (REV LTR) I
6	496.6	52.8	891 81	REXX1	V01204 Spleen necr
7	455.2	48.4	1005 81	ACRLTR1	M2223 Reticuloend
8	440.8	46.9	585 81	S82226	S82226 (RS region,
9	431.8	45.9	887 81	ACRLTR2	M2224 Reticuloend
10	425.6	45.3	1530 81	RESNVX	V01205 Spleen necr
11	307.6	32.7	859 81	REXX2	AF006066 Fowlpox v
12	160.4	17.1	1022 82	AF006066	AF006066 Fowlpox v
13	156	16.6	2640 82	AF006064	AF198100 Fowlpox v
14	155	16.6	288539 82	AF198100	AF198100 Fowlpox v
15	117.2	12.5	180 81	SNVTR	X59450 Spleen necr
16	113.6	12.1	160 4	CHKSNTIE2	M12242 Spleen necr
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18	111	11.8	160 4	CHKSNTID2	M12246 Spleen necr
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20	110.6	11.8	160 4	CHKSNTIC2	M12244 Spleen necr
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24	60.2	6.4	209 81	SNVTRMA	

[illegible]

2

LOCUS	940 bp	DNA	PAT	21-JAN-2000
DEFINITION	Sequence 1 from Patent WO9849334.			
ACCESSION	803540			

SOURCE	ORGANISM
Reticuloendotheliosis virus.	Reticuloendotheliosis virus

REFERENCE 1 (bases 1 to 940)

TITLE: NOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING SAME
 INVENTOR: DALLA, C. AND DALLA, U.
 ADDRESS: DALLA, C. AND DALLA, U.
 PATENT: WO 9849334-A 05-NOV-1998;

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Best Local Similarity	71.8%	Pred. No. 1.2e-288;		
Matches 675; Conservative	265;	Mismatches	0;	Indels 0;
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181 gaaatgucguugagcgagcaucagaccacuuagccauccaacacgagcaaacag 24

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AF006065	4292 bp	DNA	VRL	16-SEP-1997
Fowlpox virus S gag gene, complete cds, and protease/polymerase				
DEFINITION				
LOCUS				
AF006065				

ACCESSION AF006065
VERSION
AF006065.1 GI:2393892
KEYWORDS

Source: Fowlpox virus. ORGANISM: Fowlpox virus. Viruses; dsDNA viruses, no RNA stage: Poxviridae: Chordopoxvirinae:

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 4292)
Hertig, C., Coupar, B.E., Gould, A.R. and Boyle, D.B.
Field and reaction studies of fuel-rich

JOURNAL
MEDLINE
sequences from the avian retrovirus, reticuloendotheliosis virus
Virology 235 (2), 367-376 (1997)
97428585

AUTHORS. Hertig, C.H., Coupar, B.E.H., Gould, A.R. and Boyle, D.B.
TITLE. Direct Submission
JOURNAL. Submitted (30-May-1987) Division of Animal Welfare

FEATURES	FORALINGLON ROAD, GEELONG, VICTORIA 3213, AUSTRALIA
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us-09-214-124-1.rge

Page 4

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Best Local Similarity	72.3%	Pred. No. 9e-158		
Matches 39;	Conservative 146;	Mismatches		

[illegible][illegible]

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REMARK
FEATURES
source

1. (bases 1 to 545)
Retroviruses; Retroviridae; Mammalian type C
Flilado, E.J., Lee, M.F. and Humphries, E.H.
Structural genes, not the LTRs, are the primary determinants of
reticuloendotheliosis virus A-induced runting and bursal atrophy
Virology 202 (1), 116-128 (1994)
94279132
Genbank staff at the National Library of Medicine created this
entry [NCBI g1dbsg 148190] from the original journal article.
This sequence comes from Fig. 3.
Location/Qualifiers
1. .545
/organism="Reticuloendotheliosis virus"
/db_xref="taxon:11636"

[illegible]

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LOCUS		
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VERSION	S79845.1	GI:244514
KEYWORDS		
SOURCE		
	Galina	

ORANISM	Accumulated strain JM-H13 reticuloendotheliosis
REFERENCE	Gallid herpesvirus 2
AUTHORS	1 (base), dsDNA viruses, no RNA stage; Herpesviridae.
TITLE	Isfort 1 to 583)
JOURNAL	Retrovirus, Jones, D., Kost, R., Witter, R. and Kung H. J.
MEDLINE	Proc. Natl. Acad. Sci. U.S.A. 89 (3), 991-995 (1992). In vivo
REMARK	92141243
	Genbank

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FEATURES
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Db	559	GGAAGATC	566		
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DEFINITION	Reticuloendotheliosis virus 713 proviral clone RNA.				
ACCESSION	M22224 M10660 M16722				
VERSION	M22224.1 GI:209709				
KEYWORDS	long terminal repeat (LTR).				
SOURCE	Reticuloendotheliosis virus (from chicken line 151-5 B lymphomas), CDNA to mRNA, clone 713. Reticuloendotheliosis virus retroviruses; Retrovirdae; Retroviridae; Mammalian type C viruses; Retrovirus; 3-Reticuloendotheliosis virus group.				
ORGANISM	Citellus richardsoni				
REFERENCE	1 (bases 510 to 602) Ridgway,A.A., Swift,R.A., Kung,H.-J. and Fujita,D.J. In vitro transcription analysis of the viral promoter involved in c-myc activation in chicken B lymphomas: Detection and mapping of two RNA initiation sites within the reticuloendotheliosis virus long terminal repeat J. Virol. 54, 161-170 (1985)				
JOURNAL	2 (bases 1 to 887) Swift,R.A., Boerkoel,C.F., Ridgway,A., Fujita,D.J., Dodgson,J.B. and Kung,H.-J. B-Lymphoma induction by reticuloendotheliosis virus: Characterization of a mutated chicken syncytial virus provirus involved in c-myc activation J. Virol. 61, 2084-2090 (1987)				
MEDLINE	85135063				
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TITLE					
JOURNAL					
MEDLINE					
FEATURES					
source	location/Qualifiers				
LTR	/organism="Reticuloendotheliosis virus" /db_xref="taxon:11636"				
misc-feature	note="3' LTR"				
BASE COUNT	212 a 216 c 227 g 232 t				
ORIGIN	About 700 bp after segment 1.				
Query Match	45.9%; Score 431.8; DB 81; Length 887;				
Best Local Similarity	66.8%; Pred. No. 1.7e-126;				
Matches 360; Conservative 137; Mismatches 117; Indels 25; Gaps 3;					
Oy	2	augugggagggagcucucggggggaauagcgucgucgucgnaacucgccaauuagcucug	61		
Db	245	ATGTGGAGGAGGAGCTCCGGGGGAATATAGCGCTCGCTTACTGACATATATAGTTCTG	304		
Oy	62	uaauaauugcuucgucgucgcccgcgaauagacuugauuuuuuugcuugaucauauuc	121		
Db	305	TAAATCATGTTCTGCTTACCCTCCCATTTGACTTGTATATTTTCGGTCGAT-----	356		
Oy	122	ucggaucggcgaucuuucuggaucggcaucaagaagacagagcucuaauagaccuauaaag	181		
Db	357	-----ATCATTTTCTCGGAATCGGCATCAAGAGAGAGCTCATTAACCATATAAGG	405		
Oy	182	aaaugucguuaggagcagcagcacuuggccaucuugccaaucauacagagcaaacga	241		

[illegible]

[illegible]

Db	190	TTTGTTGAAGCAGACATCAGACACACTTGGACCATCTCCATATCCGAAACAAACACAGATCG	24.9
Qy	24.7	AACuauuauuacugagcccaauuguuuguaaaggcagaucuaucucccaauagaggaaau	30.6
Db	250	AACATCTCATCTAGAGCCAAATGTTGTAAAGGCAGATGCTATCTCCATAGAGGAAAT	30.9
Qy	30.7	gucaugcaacucucugucuguaaaggcgucuaauaaagccagugcaucucugcuggg	36.6
Db	310	GTCATGCAACA-----TCCTGAAGCGGCTATTAAGCCAGGTCAACTTGGTCGGGG	36.4
Qy	36.7	ucgcgcucuaacacaauuguuugacgcgcgcgcacagaauucgaucuguaaanaaaaguuu	42.6
Db	365	TCGGCGTCTCAACATTTGTTGTGACGTGCGGCCACAGATCGAATCTATATAAAG-CTT	42.3
Qy	42.7	uuucucuaauuucucgaauugacagugagaggagaaauuuuguuuguuuguuagcuggc	48.6
Db	424	TTTCTTCATATCCTCAGATTTGCAGTAGAGAGGAAATTTTGTTGCTGTGCTTGGCTGGCC	48.3
Qy	48.7	uacugugugugugugggugucggcguaauuccgaugaaauucgaucacaaau	53.9
Db	484	TACTGGGTGGGTAGGGAATCCGGAGCTGAATCCGTAAGTAATTTCCGTAAACAATTT	53.6

RESULT	7
ID	Q76038
AC	Q76038 standard; DNA; 5528 BP.
DT	20-JUL-1995 (first entry)
DE	Retrovirus vector pPoliI-R1.
KE	Retrovirus vector; pPoliI-R1; spleen necrosis virus; SNV;
KM	cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
KN	long terminal repeat; LTR; encapsidation; gene transfer;
OS	gene therapy; ss.
PN	Spleen necrosis virus.
PN	MO9429437-A.
PD	23-DEC-1994.
PF	07-JUN-1994; U06415.
PR	07-JUN-1993; US-073345.
PA	(UYNE-) UNTV NEW JERSEY.
PI	Dornburg RC;
PI	WPI; 95-035467/05.
PT	Recombinant retrovirus vector, contg. non-retroviral gene, - has
PT	ability to produce progeny virus, in helper cell which can infect
PT	host cell and form provirus
PS	Example; Page 13-14; 28pp; English.
CC	New recombination-free, highly efficient retroviral vectors
CC	pPoliI-R1 (given in Q76038), pPoliI-R2 (Q76039) and pPoliI-R3
CC	(Q76040) were obtained by replacing the U3 region of the left
CC	LTR of spleen necrosis virus with the IE promoter/enhancer of CMV
CC	and extension of the encapsidation region. The vectors allow
CC	cell-type specific gene expression and eliminate risks of
CC	downstream activation of cellular proto-oncogenes.
NO	Sequence 5528 BP; 1265 A; 1423 C; 1457 G; 1383 T;

Query Match	45.8%	Score 430.4	DB 1	Length 5528
Best Local Similarity	62.4%	Pred. No. 2.8e136		
Matches 397	Conservative 169	Mismatches 36	Indels 34	Gaps 8

Db 834 GACCTAAATCCCTAGTACTGCTGGTACAAACATTTGGGGGCTCTCGGGGATACCTCCCAT 893
 Oy 568 GCGGCGAGGUCGACUaug-----uuucucgaaucucgCGCGCGuaag-uaag 615
 Db 894 CGGCGAGAGGTCCCAACGTGCTTCTTCGAACTTTTTCGAACTCCGGCGCGGTGACTTAAg 953
 Oy 616 uacuuuauuuuuguaucucgCGaggguaauugggagaaucgga--guagCGggacgucGC 672
 Db 954 TACTTGATTGTTGTACCTCCCGAGGGGCTTTGGAGAGATCGGAGTGGGGGACCTGCC 1013
 Oy 673 GGGaagGucacacGucGCGuacagCGagggagagccGuaucugagcuc-----ug 720
 Db 1014 GGGAACTCCACCTCCGCTCAGAGAGGGAGGCCCTTACCTGAGCTCGAATTCAGATCTTG 1073
 Oy 721 uguuaucgaauguauguaugagcGucacGagcGgagaaauaauaauucuguaugug 780
 Db 1074 TGGTATCGATTGTTGTTAGACCGCTCCCTTAAGACGGTGA-TA--CTTAAGTCGTGGCTTG 1133
 Oy 781 uguuuuuuuuacucuuuguuuuuuuucuguaucuguaacGagcGccGucgaaauuguu 840
 Db 1132 TGTATTGTTGTTGCTCTGTTGTTGTTGCTCGTCGTTGTCGACAGCGGCTTCGAAATTGGTCT 1199
 Oy 841 gcccaccccgCGgGgucuuugGgaauaauacuuugagagucuuuuugcucacagugucucc 900
 Db 1192 ACCCACACCGGGGGCTTGGGAATAATATTGGAAGAGCTTTGCTCCACAGTGTCTTC 1251
 Oy 901 guuuuacugucucucucucucucucucgagcgagga 936
 Db 1252 GTCGTACTGCTCCTCCTCTCCCTCTCCGCGCGGGA 1287

RESULT 8
076039
ID 076039 standard; DNA; 5525 BP.
AC 076039;
DT 20-JUL-1995 (first entry)
DE Retrovirus vector pPoli1-R2.
KW Retrovirus; vector; pPoli1-R2.
KW cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
KW long terminal repeat; LTR; encapsidation; gene transfer;
KW gene therapy; ss.
OS Spleen necrosis virus.
PN MO9429437-A.
PD 22-DEC-1994.
PD 07-JUN-1994; U06415.
PR 07-JUN-1993; US-073345.
PA (UYNE-) UNIV NEW JERSEY.
PI Dornburg RC.
DR WPI: 95-036467/05.
PT Recombinant retrovirus vector; contg. non-retroviral gene, - has
PT ability to produce progeny virus, in helper cell which can infect
PT host cell and form provirus
PS Example; Page 14-16; 28pp; English.
CC New recombination-free, highly efficient retroviral vectors
CC pPoli1-R1 (given in Q76038), pPoli1-R2 (Q76039) and pPoli1-R3
CC (Q76040) were obtained by replacing the U3 region of the left
CC LTR of spleen necrosis virus with the IE promoter/enhancer of
CC and extension of the encapsidation region. The vectors allow
CC cell-type specific gene expression and eliminate risks of
CC downstream activation of cellular proto-oncogenes.
SO Sequence 5525 BP; 1264 A; 1422 C; 1457 G; 1382 T;

Query Match	44.7%	Score	420	DB 1	Length	5525			
Best Local Similarity	62.7%	Prod. NO.	9.9e-133						
Matches	386	Conservative	166	Mismatches	30	Indels	34	Gaps	8

[illegible]

Db	731	TCGTGTAATAAACTTTTTCCTTCGATTCCTCAATTCGACAGTGGAGGAGATTTTGT	790
Qy	470	cgagguuagagcgccuacugugugug- guagggugccggagcuagauuc	528
Db	791	CGTGGTGTCCCTGCGCTACTGGGTGGGGCGAGGATCCGGATCGAACTCTACTTCTC	850
Qy	529	gaacaaacuuaggggcuucucgggga- uccucccaucggaggaugcuacug-	585
Db	851	GGTACAACTTGTGGGGCTGTCCGGATACCTTCCATCGCAGAGGTCCAACTGCT	910
Qy	586	-----uuuuuugaacucucggcgccguaa- uaaguacuuuuuugaucucg	635
Db	911	TCCTCGAATCTTCTCGAATCCGGCGCGGAGTAACTGATTGTGTACTCG	970
Qy	636	cgaggguuaggagagucga--- guggggagacgucggggagcucaacucguc	692
Db	971	CGAGGGTTTGGGAGATCGGAGTGGTGGCGGAGCCTCGCGGAAAGCTCACCTCGCTC	1030
Qy	693	agcagggagcccgucuuacugacuc----- uguuuuacuuuuuguuug	740
Db	1031	AGCAGGGGAGCCCTACTACCTGACCTCGAATTCAGATCTTGCTATCTGATGTGTGA	1090
Qy	741	accgucuccaagcgcgugauaauaauagucguguuuguuuguuuuuacucug	800
Db	1091	GCCCTCCCTTAAGACGGGATTA-- CTAAGTCGTGGCTGTGTGTGTGTGTGTGCTTGTG	1148
Qy	801	uuuuuuugucacuuugucagacagcccgucggaauuguuuguccacacgcgcgucuc	860
Db	1149	TTTCTTGCTGCTTGTGACAGCGCCTTGCGAATTGTGTATCCACACCGCGGCTTGC	1208
Qy	861	gaauaauuuuaggagagucuuuugccuacagugucucgguuacucgucucucuc	920
Db	1209	GAATAAATACCTTGGAGAGCCTTTGCTCCAGTGTCTTCGCTGTACTGTCCTCTCT	1268
Qy	921	ccucucucgcccggga 936	
Db	1269	CCCTCTCCGCGCGGGA 1284	
RESULT	9		
ID	076040	standard; DNA; 5519 BP.	
AC	076040:		
DE	20-JUL-1995	(first entry)	
DE	Retrovirus vector pPoli1-R3.		
KV	Retrovirus; vector; pPoli1-R3; spleen necrosis virus; SNV;		
KV	cytomagalovirus; CMV; intermediate-early promoter; IE promoter;		
KV	long terminal repeat; LTR; encapsidation; gene transfer;		
KV	gene therapy; ss.		
OS	Spleen necrosis virus.		
PN	W09429437-A.		
PF	22-DEC-1994.		
PR	07-JUN-1994; U06415.		
PR	07-JUN-1993; US-073345.		
PA	(UYNE-) UNIV NEW JERSEY.		
PI	Dornburg RC;		
PI	WPI: 95-036467/05.		
PT	Recombinant retrovirus vector, contg. non-retroviral gene, - has		
PT	ability to produce progeny virus, in helper cell which can infect		
PT	host cell and form provirus		
PS	Example; Page 16-17; 28pp; English.		
CC	New recombinant-free, highly efficient retroviral vectors		
CC	pPoli1-R1 (given in 076038), pPoli1-R2 (076039) and pPoli1-R3		
CC	(076040) were obtained by replacing the U3 region of the left		
CC	LTR of spleen necrosis virus with the IE promoter/enhancer of CMV,		
CC	and extension of the encapsidation region. The vectors allow		
CC	cell-type specific gene expression and eliminate risks of		
CC	downstream activation of cellular proto-oncogenes.		
SO	Sequence 5519 BP: 1264 A; 1420 C; 1456 G; 1379 T;		

[illegible]

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 09:13:46 ; Search time 172.61 Seconds
(without alignments)
749.102 Million cell updates/sec

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Title: US-09-214-124-1
Perfect score: 940
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Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

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Minimum DB seq length: 0
Maximum DB seq length: 1000000

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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

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5: /c9n2_6/prodata_1/1na/6-COMB.seq:*
6: /c9n2_6/prodata_1/1na/PTCUS-COMB.seq:*
7: /c9n2_6/prodata_1/1na/backfiles1.seq:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			ID	Description
		Match	Length	DB		
C 2	37.6	4.0	7218	1	US-08-332-463-14	Sequence 14, Appl
	30.6	3.3	1276	4	US-08-793-599-1	Sequence 1, Appl
	30.6	3.3	2142	4	US-08-793-599-3	Sequence 3, Appl
C 4	29	3.1	13158	4	US-08-687-080-105	Sequence 105, App
C 5	28.8	3.1	3934	5	US-09-226-568-18	Sequence 18, Appl
C 6	28.8	3.1	3946	5	US-08-077-4848-1	Sequence 1, Appl
C 7	28.8	3.1	3946	5	US-09-211-640-1	Sequence 1, Appl
C 8	28.8	3.1	3946	6	PCT-US91-03547-1	Sequence 1, Appl
C 9	28.8	3.1	11531	1	US-08-068-945A-1	Sequence 1, Appl
10	28.8	3.1	11531	2	US-08-442-806-1	Sequence 1, Appl
11	28.2	3.0	221	1	US-08-232-177A-17	Sequence 17, Appl
12	28.2	3.0	278	1	US-08-232-177A-52	Sequence 52, Appl
13	28.2	3.0	278	1	US-08-333-170B-1	Sequence 1, Appl
C 14	28.2	3.0	9636	2	US-08-162-081B-34	Sequence 34, Appl
15	28	3.0	3240	2	US-08-162-081B-34	Sequence 34, Appl
16	28	3.0	3240	2	US-08-760-872-34	Sequence 32, Appl
17	28	3.0	3412	2	US-08-162-081B-32	Sequence 32, Appl
18	28	3.0	3412	3	US-08-760-872-32	Sequence 30, Appl
19	28	3.0	246240	3	US-08-724-394A-20	Sequence 20, Appl
20	28	3.0	246240	3	US-08-724-394A-21	Sequence 21, Appl
21	28	3.0	246240	3	US-08-724-394A-22	Sequence 22, Appl
22	27.8	3.0	1391	1	US-08-261-662-1	Sequence 1, Appl
23	27.8	3.0	1391	6	PCT-US95-07752-1	Sequence 1, Appl
C 24	27.6	2.9	3565	5	US-08-689-421-32	Sequence 32, Appl
C 25	27.6	2.9	6545	4	US-08-843-530B-1	Sequence 1, Appl
C 26	27.6	2.9	8224	4	US-09-010-398-14	Sequence 14, Appl
C 27	27.6	2.9	10603	5	US-09-080-044-1	Sequence 1, Appl

27	27.4	2.9	943	5	US-08-705-875A-1	Sequence 1, Appl1
28	27.2	2.9	2055	1	US-07-842-34.9-1	Sequence 1, Appl1
29	27.2	2.9	2277	2	US-08-676-967-2	Sequence 2, Appl1
30	27.2	2.9	2277	2	US-08-676-974-2	Sequence 2, Appl1
31	27.2	2.9	2277	4	US-09-098-487-2	Sequence 2, Appl1
32	27.2	2.9	2643	4	US-08-781-802-11	Sequence 11, Appl1
33	27.2	2.9	3355	3	US-08-916-917-11	Sequence 11, Appl1
34	27.2	2.9	3355	5	US-09-225-170-11	Sequence 11, Appl1
35	27.2	2.9	3355	4	US-08-781-802-9	Sequence 9, Appl1
36	27.2	2.9	3826	4	US-08-731-722-1	Sequence 2, Appl1
37	27.2	2.9	3826	4	US-08-731-722-2	Sequence 2, Appl1
38	27.2	2.9	3826	4	US-08-731-722-3	Sequence 3, Appl1
39	27.2	2.9	4315	5	US-08-781-802-1	Sequence 1, Appl1
40	27.2	2.9	7308	4	US-09-166-186-107	Sequence 107, Appl1
41	27.2	2.9	741	5	US-08-937-271-12	Sequence 12, Appl1
42	27	2.9	1029	5	US-08-937-271-16	Sequence 16, Appl1
43	27	2.9	2281	2	US-08-164-614A-1	Sequence 1, Appl1
44	27	2.9	2281	4	US-08-456-489B-1	Sequence 1, Appl1
45	27	2.9	2281	6	PCT-US03-01720-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463

GENERAL INFORMATION:

TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52

STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria

```

; OF LINEAGE COUNTRY :
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 14:

US-08-232-463-14

[illegible]

RESULT 2
 : US-08-793-599-1/C
 : Sequence 1, Application US/087935599
 : Patent No. 5952489
 :
 : GENERAL INFORMATION
 :
 : APPLICANT: OKADA, YUKIO
 : APPLICANT: YOSHIGI, NAOHIRO
 : APPLICANT: ITO, KAZUTOSHI
 : APPLICANT: KIHARA, MAKOTO
 :
 : TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
 :
 : FILE REFERENCE: 2589-0056-0 PCT
 : CURRENT APPLICATION NUMBER: US/08/793,599
 : CURRENT FILING DATE: 1997-03-04
 : EARLIER APPLICATION NUMBER: PCT/JP96/01866
 : EARLIER FILING DATE: 1996-07-05
 : EARLIER APPLICATION NUMBER: JP 191028/1995
 : EARLIER FILING DATE: 1995-07-05
 :
 : NUMBER OF SEQ ID NOS: 3
 :
 : SOFTWARE: PatentIn Ver. 2.0
 :
 : SEQ ID NO 1
 :
 : LENGTH: 1276
 :
 : TYPE: DNA
 :
 : ORGANISM: Barley
 :
 : US-08-793-599-1

	Query Match	3.38;	Score 30.6;	DB 4;	Length 1276;	
	BEST Local Similarity	27.18;	Pred. NO. 1.4;			
	Matches	23;	Conservative	28;	Mismatches	34; Indels 0; Gaps 0;
QY	aauuguuuguagaccgucuccaaagaoguguaanaaagucguuuuguuuguuunuu	789				
DG	:::::-::: :::- :: :::- :::- :::- :::- :::- :::- :::- :::-					
DG	ATTATATTCAACAGTGTCCACTAGAGTTCAAGTCCTCAGACTTGATTCGGTTGCCA	77				
QY	guaacccuuuguuuuuugucacuu	814				
DG	::: :::~::~-:::~:: ::-					
DG	GTTTCCTTAATTATTTCATGCCTT	52				

RESULT 3
US-08-793-599-3/C
Sequence 3, Application US/08/935599
Patent No. 5952489
GENERAL INFORMATION:
APPLICANT: OKADA, YUKIO
APPLICANT: YOSHIDA, NAOHITO
APPLICANT: ITO, KAZUTOSHI

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? APPLICANT: KIHARA, MAKOTO
? TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
? FILE REFERENCE: 2589-0056-0 PCT
? CURRENT APPLICATION NUMBER: US/08/793, 599
? CURRENT FILING DATE: 1997-03-04
? EARLIER APPLICATION NUMBER: PCT/JP96/01866
? EARLIER FILING DATE: 1996-07-05
? EARLIER APPLICATION NUMBER: JP 191028/1995
? EARLIER FILING DATE: 1995-07-05
? NUMBER OF SEQ ID NOS: 3
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 3
? LENGTH: 2142
? TYPE: DNA
? ORGANISM: Batley
US-08-793-599-3

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	Query Match	3.3%	Score 30.6;	DB 4;	Length 2142;
	Best Local Similarity	27.1%;	Pred. No.1.9;		
	Matches	23;	Conservative	28;	Mismatches 34; Indels 0; Gaps 0;
OY	730	aauuguuugugacgucnucncagcaagaaguganaaanaagucuguguuuguuugunuu	789		
		::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::			
Dd	136	atttattttcttaaacgcgtcactctaagtccaatgaagttccagtccttgattgtttggcaa	77		
OY	790	guuaaccuuguuuuugucgacaau	814		
		::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::			
Dd	76	grrtcctttaattatttcattgcctt	52		

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: RESULT 4
: US-08-687-080-105/c
: Sequence 105, Application US/08687080
: Patent No. 5965427
: GENERAL INFORMATION:
: APPLICANT: Gregory Dolganov
: TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
: NUMBER OF SEQUENCES: 175
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dehlinger & Associates
: STREET: 350 Cambridge Avenue, Suite 250
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94306
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/687,080
: FILING DATE: 17-JUL-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/592,126
: FILING DATE: 26-JAN-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sholtz, Charles K.
: REGISTRATION NUMBER: 38,615
: REFERENCE/DOCKET NUMBER: 4600-0111.30
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 324-0880
: TELEFAX: (415) 324-0960
: INFORMATION FOR SEQ ID NO.: 105:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13158 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 3946 base pairs
: type: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: IMMEDIATE SOURCE:
: CLONE: mcl-1
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 61..1110 /note= "when nucleotide 740 = C,
: OTHER INFORMATION: amino acid 227 = A; when nucleotide 740 = T, amino
: OTHER INFORMATION: acid 227 = V."
US-09-211-640-1

Query Match 3.18; Score 28.8; DB 5; Length 3946;
Best Local Similarity 56.28; Pred. No. 11;
Matches 27; Conservative 9; Mismatches 12; Indels 0; Gaps

Oy 887 GACGCGUACUCCGUGUACUGUCCUCCUCCUCCUCCUCCGCGCG 934
|:||||| |:|||: |:|||||:| |:|:| ||||
Db 600 CTCACGCGACTGCGGTACAACACTCTCTCTCTCTCTCTGCGG 553

RESULT 8
PCT-US94-03547-1/c
: Sequence 1, Application PC/TUS9403547
: GENERAL INFORMATION:
: APPLICANT: The Johns Hopkins University School of Medicine
: TITLE OF INVENTION: MYELOID CELL LEUKEMIA ASSOCIATED GENE
: TITLE OF INVENTION: MCL-1
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Spensley Horn Jubas & Lubitz
: STREET: 1880 Century Park East, Suite 500
: CITY: Los Angeles
: STATE: California
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/03547
: FILING DATE: 31-MAR-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Wetherell, Jr., Ph.D., John W.
: REGISTRATION NUMBER: 31,678
: REFERENCE/DOCKET NUMBER: FD-2845
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 455-5110
: TELEFAX: (619) 455-5110
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3946 base pairs
: type: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: IMMEDIATE SOURCE:
: CLONE: mcl-1
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 61..1110 /note= "when nucleotide 740 = C,
: OTHER INFORMATION: amino acid 227 = A; when nucleotide 740 = T, amino
: OTHER INFORMATION: acid 227 = V."
: PCT-US94-03547-1

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Query Match 3.1%; Score 28.8; DB 6; Length 3946;
Best Local Similarity 56.2%; Pred. No. 11;
Matches 27; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 887 caccagucucucgguuugacucgucucucucucgagcg 934
      1:||||| 1: 1: 1: 1:1:1:1:1:1: 1:1: 1: 1:1
Db 600 CTCACGACATGCCGATACAACTCTCTCTCTCTCTGCTGCGG 553

RESULT 9
US-08-068-945A-1
; Sequence 1, Application US/08068945A
; Patent No. 5616483
; GENERAL INFORMATION:
; APPLICANT: Bjursell, Gunnar
; APPLICANT: Carlsson, Peter
; APPLICANT: Enerback, Sven
; APPLICANT: Hansson, Lennart
; APPLICANT: Lidberg, Ulf
; APPLICANT: Nilsson, Jeanette
; APPLICANT: Tornell, Jan
; TITLE OF INVENTION: New DNA Sequences
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068, 945A
; FILING DATE: 27-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201809-2
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201826-6
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9202088-2
; FILING DATE: 03-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300902-5
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Mammary gland
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1653..1727, 4071..4221, 4307..4429, 4707

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					Gaps
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Db	55	AGGAAATGTTGTGTGTTGAAATCACTGATGACATGACATATATATACGTGTGTGTGTG	114		
Oy	785	uguuuuuacuu	821		
				
Db	115	TGT	151		

[illegible]

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1 ADDRESS:EE: Felte & Lynch
2 STREET: 805 Third Avenue
3 CITY: New York
4 STATE: New York
5 COUNTRY: USA
6
7 ZIP: 10022
8
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
11 COMPUTER: IBM PS/2
12 OPERATING SYSTEM: PC-DOS
13 SOFTWARE: Wordperfect
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/162.081B
16 FILING DATE: February 7, 1994
17
18 CLASSIFICATION: 435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: PCT/GB93/00761
21 FILING DATE: 13 April 1993
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Pascualini, Patricia A.
24 REGISTRATION NUMBER: 34,894
25 REFERENCE/DOCKET NUMBER: LUD 5256
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (212) 688-9200
28 TELEFAX: (212) 838-2884
29 INFORMATION FOR SEO ID NO: 34:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 3240 base pairs
32 TYPE: nucleic acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35
36 JS-08-162-081B-34

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1 ADDRESSSEE: Felfe & Lynch
2 STREET: 805 Third Avenue
3 CITY: New York
4 STATE: New York
5 COUNTRY: USA
6 ZIP: 10022
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Diskette, 5.25 Inch, 360 kb storage
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11 OPERATING SYSTEM: PC-DOS
12 SOFTWARE: Wordperfect
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22 FILING DATE: 13 April 1993
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24 ATTORNEY/AGENT INFORMATION:
25 NAME: Pasqualini, Patricia A.
26 REGISTRATION NUMBER: 34,894
27 REFERENCE/DOCKET NUMBER: LUD 5256
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (212) 688-9200
30 TELEFAX: (212) 838-3884
31
32 INFORMATION FOR SEQ ID NO: 34:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 3240 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38
39 JS-08-162-081B-34

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 09:13:46 ; Search time 3871.63 seconds
(without alignments)
1070.670 Million cell updates/sec

Title: US-09-214-124-1
Perfect score: 940
Sequence: 1 aaugugggagggagcuccgg.....ccucuccggccgggauggg 940

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues
Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: em_est2:*
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115: em_gss12:*
116: gb_gss12:*

[illegible][illegible]

[illegible][illegible]

SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila..
REFERENCE 1 (bases 1 to 1159)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr)

COMMENT

FEATURES
source location/Qualifiers
1..1159
/organism="Drosophila melanogaster"
/plasmid="pbeloBAC11"
/db_xref="taxon:7227"
/clone_1id="DrosBAC"
/clone="BACN15017"
/note="end : 17"
/note="end : 17"

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ORIGIN

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Best Local Similarity 3.7%; Pred. No. 0.35;
Matches 15; Conservative 230; Mismatches 161; Indels 1; Gaps 1

OY 530 aaacacaauuggggagcucgcgcgggaauuccucccaacgcgcagaagucuaucguuuuc 589
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 676 ATDCWMCCTTATTAATAAATGTTAAKMBTBCKCAAVDTCDYGTTBTBTSTKTSTBSBV 735
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
OY 590 uucgacacucgcgcgcgcgaagaaagacuauguuugacucgcgcgcaggguuuuggag 649
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 736 NAYRASAMTKMTADAKSTBKMATLAANTSTTBTSSTBSBYSTBPBYSTDYKYK 795
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OY 650 gaucggaugcgcgagccgcgcgcgggaaguccaccucgcgcagcaggggagcccuga 709
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 736 BBTBTBMSWTATTATATAATSCSTSBSSSSSTBSBGCKSTGSTSSBABRTSVTK 855
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
OY 710 uuugagcuuuguguaucuauguuuguuugacucgcgcuccaagcggugauaanaug 769
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 856 TGTSTSBCTBTBTBYSBTSTBSBBBTDDBASTITKBSTSTBSTSTSTSTSTSTST 915
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OY 770 cguguuuguguuuguuuguaucucuuuguuuguuuguc acuuugcacagcgccu 828
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 916 STTST 975
|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
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|:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 976 SSSBSSTSSBSBBBKTBTSTGSTSTSBSTSTSTSTSTSTSTSTSTSTSTSTSTST 1035
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OY 889 ccaguguuucgguuugacucgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcg 935
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RESULT 7
CNSOL6TE
LOCUS CNSOL6TE 1010 bp DNA GSS 26-JUL-1999
DEFINITION Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN1505 of DrosBAC library from Drosophila melanogaster (fruit
fly) genomic survey sequence.
AL107180
VERSION AL107180.1 GI:5626016
KEYWORDS GSS.

[illegible]

project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES	Location/Qualifiers
Source	1. .1201

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/organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
/clone_1lb="DrosBAC"
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ORIGIN					

Query Match	3.9%;	Score 36.4;	DB 123;	Length 1201;
Best Local Similarity	11.7%;	Pred. NO. 2.5;		
Matches 45;	Conservative 149;	Mismatches 191;	Indels 0;	Gaps 0

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Oy      423 uuuuuuuucuaaucauccacagaauggcaggagaaguuuuuugaucgugugaugagcc  
          :::: :|:: : : : |:: :|: : |:|: :||:  
  
Db      686 tyytttcyyttaadkgnadnwnknsmckrhngsrcgttctcgttttgtgccck
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Qy 483 ggcuaacuggggguaggggucaggaaucgugaauuuugaaacaacuuugg 542
| : : ||| | : : : : :
Db 746 wggggctcttttgcTTTTYTBGGGGGGGCTTTTKSSCnTTTTTTTTTBCfCCCGSGGGGG 805

Oy	543	gggcugucgaggaauccucccaacgscagaagugcuaucguuuucucgaaucgcgc	602
		: :	:
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[illegible]

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      : | : ||| : : : | : : ||| : : : :
Db 926 SCCCTTTTSGGGCCTGTTBTKBGBGYCCSSSSSGSSGSKBYSCSCTCYYYTITTTTTTCTT 985
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QY 723 guaacugaaugaaugacacccgucuccaagacgugaaauaauaagucuguguaugugug 702

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Dy 783 aaagaauguaaccugugaauguc 807
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Search completed: August 7, 2000, 11:56:02

job time: 9/30 sec

Tue Aug 8 08:33:20 2000

us-09-214-124-2.rst

Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 11:56:02 ; Search time 3871.63 Seconds
(without alignments)
658.348 Million cell updates/sec

Title: US-09-214-124-2
Perfect score: 578
Sequence: 1 ggggucgcgcgcucacacau.....ccucucgcgcgggauggg 578

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues 10495684

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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[illegible]

	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
	l (bases 1 to 884)				
	Genoscope.				
	Direct Submission				
	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :				
	Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr				
	- Web : www.genoscope.cns.fr)				
	Determination of this BAC-end sequence was carried out as part of a				
	collaboration with the Berkeley Drosophila Genome Project (BDGP).				
	The BDGP is constructing a physical map of the Drosophila				
	melanogaster genome using these BACs. For further information				
	please see http://www.fruitfly.org/The_BDGP_Drosophila				
	Melanogaster BAC library was prepared by Kazutoyo Osogawa and				
	Aaron Mamosser in Pieter de Jong's laboratory in the Department of				
	Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,				
	NY. The library is named RPCI-98 and was constructed by partial				
	ECORI digestion of Drosophila DNA provided by the BDGP from the				
	isogenic strain y2; cn bw sp, the same strain used for the BDGP's				
	p1 and EST libraries. A more detailed description of the library				
	and how to order individual BAC clones, the entire library, or				
	filters for hybridization from the BACPAC Resource Center can be				
	found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .				
	location/Qualifiers				
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	/clone_1lb="RPCI-98"				
	/clone="BACRI4N21"				
	/note="end : T7"				
BASE COUNT	230 a 220 c 139 g 124 t 329 others				
ORIGIN					

[illegible]

[illegible][illegible]

Tue Aug 8 08:33:20 2000

us-09-214-124-2.rst

RESULT 3
US-08-793-599-3/c
; Sequence 3, Application US/087935599
; Patent No. 5952489
; GENERAL INFORMATION:
; APPLICANT: OKADA, YUKIO
; APPLICANT: YOSHIGI, NAOKIHO
; APPLICANT: ITO, KAZUTOSHI

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1      RESULT      4
2      US-08-687-080-105/C
3      : Sequence 105, Application us/08687080
4      : Patent No. 5965427
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Gregory Dolganov
8      : TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
9      : NUMBER OF SEQUENCES: 175
10     : CORRESPONDENCE ADDRESS:
11     : ADDRESSEE: Dehlinger & Associates
12     : STREET: 350 Cambridge Avenue, Suite 250
13     : CITY: Palo Alto
14     : STATE: CA
15     : COUNTRY: USA
16     : ZIP: 94306
17     : COMPUTER READABLE FORM:
18     : MEDIUM TYPE: Floppy disk
19     : COMPUTER: IBM PC compatible
20     : OPERATING SYSTEM: PC-DOS/MS-DOS
21     : SOFTWARE: Patentln Release #1.0, Version #1.25
22     :
23     : CURRENT APPLICATION DATA:
24     : APPLICATION NUMBER: US/08/687,080
25     : FILING DATE: 17-JUL-1996
26     : CLASSIFICATION: 435
27     :
28     : PRIOR APPLICATION DATA:
29     : APPLICATION NUMBER: US 08/592,126
30     : FILING DATE: 26-JAN-1996
31     :
32     : ATTORNEY/AGENT INFORMATION:
33     : NAME: Sholtz, Charles K.
34     : REGISTRATION NUMBER: 38,615
35     : REFERENCE/DOCKET NUMBER: 4600-0111.30
36     : TELECOMMUNICATION INFORMATION:
37     : TELEPHONE: (415) 324-0880
38     : TELEFAX: (415) 324-0960
39     :
40     : INFORMATION FOR SEQ ID NO: 105:
41     : SEQUENCE CHARACTERISTICS:
42     : LENGTH: 13158 base pairs
43     : TYPE: nucleic acid
44     : STRANDEDNESS: double
45     : TOPOLOGY: linear
46     :
47     : MOLECULE TYPE: DNA (genomic)
48     :
49     : HYPOTHETICAL: NO

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SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: mcl-1
FEATURE:
NAME/KEY: CDS
LOCATION: 61..1110
OTHER INFORMATION: /note= "when nucleotide 740 = C,
OTHER INFORMATION: amino acid 227 = A; when nucleotide 740 = T, amino
OTHER INFORMATION: acid 227 = V."
US-09-211-640-1

Query Match          5.0%; Score 28.8; DB 5; Length 3946;
Best Local Similarity 56.2%; Pred. No. 8.1;
Matches 27; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 525 cuccagugucucgguuuuagucucucucucucucucgagcg 572
Db 600 CTCACGCGACTGCCGATACACTGCTCTCTCTCTCTCTGCGCG 553

RESULT 8
PCT-US94-03547-1/C
; Sequence 1, Application PC/TUS9403547
; GENERAL INFORMATION:
; APPLICANT: The Johns Hopkins University School of Medicine
; TITLE OF INVENTION: MYELOID CELL LEUKEMIA ASSOCIATED GENE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Juras & Lubitz
; STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/03547
; FILING DATE: 31-MAR-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-2845
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3946 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: mcl-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 61..1110
; OTHER INFORMATION: /note= "when nucleotide 740 = C,
; OTHER INFORMATION: amino acid 227 = A; when nucleotide 740 = T, amino
; OTHER INFORMATION: acid 227 = V."
PCT-US94-03547-1
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Best Local Similarity 56.2%; Pred. No. 8.1;
Matches 27; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 525 cuccagugucucgguuuuagucucucucucucucgagcg 572
Db 600 CTCACGCGACTGCCGATACACTGCTCTCTCTCTCTCTGCGCG 553

RESULT 9
US-08-068-945A-1
; Sequence 1, Application US/08068945A
; Patent No. 5616483
; GENERAL INFORMATION:
; APPLICANT: Bjursell, Gunnar
; APPLICANT: Carlsson, Peter
; APPLICANT: Enerback, Sven
; APPLICANT: Hansson, Lennart
; APPLICANT: Lidberg, Ulf
; APPLICANT: Nilsson, Jeanette
; APPLICANT: Tornell, Jan DNA Sequences
; TITLE OF INVENTION: New DNA Sequences
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/068,945A
; FILING DATE: 27-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201809-2
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201826-6
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9202088-2
; FILING DATE: 03-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300902-5
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Steiner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; TELEFAX: (212)354-8113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11531 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: -DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Mammary gland
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1653..1727, 4071..4221, 4307..4429, 4707
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LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11394)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: join(1722..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11394)
OTHER INFORMATION: /EC_number= 3.1.1.1
OTHER INFORMATION: /product= "Bile Salt-stimulated Lipase"
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..1640
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NAME/KEY: TATA_signal
LOCATION: 1611..1617
FEATURE:
NAME/KEY: exon
LOCATION: 1641..1727
FEATURE:
NAME/KEY: exon
LOCATION: 4071..4221
FEATURE:
NAME/KEY: exon
LOCATION: 4307..4429
FEATURE:
NAME/KEY: exon
LOCATION: 4707..4904
FEATURE:
NAME/KEY: exon
LOCATION: 6193..6323
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NAME/KEY: exon
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FEATURE:
NAME/KEY: exon
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NAME/KEY: exon
LOCATION: 8335..8521
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NAME/KEY: exon
LOCATION: 8719..8922
FEATURE:
NAME/KEY: exon
LOCATION: 10124..10321
FEATURE:
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FEATURE:
NAME/KEY: 3'UTR
LOCATION: 11491..11531
US-08-068-945A-1

Query Match 5.0%; Score 28.8; DB 1; Length 11531;
Best Local Similarity 33.6%; Pred. No. 14;
Matches 51; Conservative 24; Mismatches 77; Indels 0; Gaps 0;

QY 305 gcugcgggaagcuccacccgucagcaggggagcccgucagucuguguguan 364
DB 7107 GCTGACGTGCAACCTCCACCTCGGGTTCAAGTATCTGTGACTCACTCCAGTGTAG 7166
QY 365 cugauuguuugugucgucgucgucagagcguguaauaauaagucguguuuguuug 424
DB 7167 CTGGGACTACAGCAGCATGCCACCATGCCAGATTAATTTTCTGTGTAGTAGGAT 7226
QY 425 uuuguaacuguguuugucgucacugucug 456
DB 7227 GGAGTTTATCTGTGTAGTAGGATGATCTGC 7258
RESULT 10
US-08-442-806-1

Sequence 1, Application US/08442806
Patent No. 5716817
GENERAL INFORMATION:
APPLICANT: Bjursell, Gunnar
APPLICANT: Carlsson, Peter
APPLICANT: Enerback, Sven
APPLICANT: Hansson, Lennart
APPLICANT: Lidberg, Ulf
APPLICANT: Nilsson, Jeanette
APPLICANT: Tornell, Jan
TITLE OF INVENTION: Genomic DNA Sequences
TITLE OF INVENTION: Encoding Human BSSL/CEL
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,806
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,945
FILING DATE: 27-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: join(1653..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11394)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: join(1722..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11394)
OTHER INFORMATION: /EC_number= 3.1.1.1

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Best Local Similarity 33.6%; Pred. No. 14;
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QY      365 cugauuuuguuugagaccguccuaagcagcygugauaanaaagucyguuuuguuuguyug 424
           ||| : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7167 CTGGGACTACAAAGGCACATGCCACCATGCCAATATTATTTTCTGTGTATTAGAGGAT 7226

QY      425 uuuguuacuuguguuuguugucacucungug 456
           ||| : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      7227 GGAGTTTCATCGTTTAGCTAGATGATCTCG 7258

RESULT 11
US-08-222-177A-17
; Sequence 17, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n..(dc-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
;
```

ADDRESS: Demitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Caucasian
TISSUE TYPE: Blood
IMMEDIATE SOURCE:
CLONE: M130
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 3
FEATURE:
NAME/KEY: repeat.region
LOCATION: 103..139 /rpt_type= "tandem"
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NAME/KEY: misc.feature
LOCATION: 77..91
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OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc.feature
LOCATION: complement (144..163)
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OTHER INFORMATION: /citation= ([1])
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NAME/KEY: misc.feature
LOCATION: 1..221
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OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Only one strand sequenced"
PUBLICATION INFORMATION:
AUTHORS: Weber, J. L.
AUTHORS: May, P. E.
TITLE: Dinucleotide repeat polymorphism at the
TITLE: D3S240 locus
JOURNAL: Nucleic Acids Res


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; FILING DATE: 09-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/162,081
; FILING DATE: February 7, 1994
; APPLICATION NUMBER: PCT/GB93/00761
; FILING DATE: 13 April 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD 5256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-780-872-34

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Query Match
Best Local Similarity 4.8%; Score 28; DB 3; Length 3240;
Matches 26; Conservative 20; Mismatches 30; Indels 0; Gaps 0;

Qy 404 aagucguguguuuguguuuguuuacucuguguuugucgucacugucgacagcgc 463
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Db 2475 AATCAAGCTCTGATCTCGAATGTTACTTATGTTGTCTGTCATCGTGACTGTGT 2534
    ||:| ||:| :|:| :|:| ||:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Qy 464 ccugcgaaugugug 479
    ||:| ||:| :|:| :|:| ||:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|
Db 2535 GGCCTTATGAGTGTG 2550
    ||:| ||:| :|:| :|:| ||:| :|:| :|:| :|:| :|:| :|:| :|:| :|:|

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Search completed: August 7, 2000, 09:28:43
 Job time: 897 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 10:53:33 ; Search time 4994.97 Seconds
(without alignments)
1200.515 Million cell updates/sec

Title: US-09-214-124-2
Perfect score: 578
Sequence: 1 ggggucgcgcgcacacau.....ccucucgcgcgcgauggg 578

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 5187315402 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_dal: *
2: gb_dal2: *
3: gb_cm: *
4: gb_ov: *
5: gb_pat: *
6: gb_ph: *
7: gb_pl1: *
8: gb_pl2: *
9: gb_pr1: *
10: gb_pr2: *
11: gb_pr3: *
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13: gb_sts: *
14: gb_sy: *
15: gb_un: *
16: em_fun: *
17: em_hum1: *
18: em_hum2: *
19: em_in: *
20: em_om: *
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23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_sy: *
29: em_un: *
30: em_v1: *
31: gb_htg1: *
32: gb_htg2: *
33: gb_in1: *
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38: em_hum4: *
39: gb_pr4: *
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65: em_htg7: *
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79: gb_htg30: *
80: gb_htg31: *
81: gb_v11: *
82: gb_v12: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	423.6	73.3	1530	81	RESNVX
5	310	53.6	891	81	REXXK1
6	173.4	30.0	1005	81	ACRUTR1
7	171	29.6	545	81	S70398
8	156.4	27.1	585	81	S82226
9	153	26.5	583	81	S79845
10	150	26.0	887	81	ACRUTR2
11	121	20.9	859	81	REXXK2
12	113.6	19.7	160	4	CHRSNVF2
13	113	19.6	180	81	SNVTR
14	111.6	19.3	160	4	CHRSNVB2
15	111	19.2	160	4	CHRSNVB2
16	111	19.1	160	4	CHRSNVF2
17	110.6	19.1	160	4	CHRSNVF2
18	110.6	19.1	160	4	CHRSNVF2
19	110.6	19.1	160	4	CHRSNVF2
20	110.6	19.1	160	4	CHRSNVF2
21	110.6	19.1	160	4	CHRSNVF2
22	110.6	19.1	160	4	CHRSNVF2
23	110.6	19.1	160	4	CHRSNVF2
24	110.6	19.1	160	4	CHRSNVF2

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09 124 124 124 124 124

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[illegible]

RESULT 4
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ID Q76041 standard; DNA; 3878 BP.
AC Q76041;
DT 20-JUL-1995 (first entry)
DE Retrovirus vector pPOL15-R1
KW Retrovirus; vector; pPOL15-R1
KW gene transfer; gene therapy; ss.
KW Salcom necrosis virus.
PN K09428437-RI
PD 22-DBS-49994
PF 07-JUN-1994; U0641E.
PR 07-JUN-1993; US-073345.
RA (VYNE-) UNIV. NEW JERSEY.
DR WPI: 95-036467/05.
PT Recombinant retrovirus vector, contg. non-retroviral gene, - has
PT ability to produce progeny virus, in helper cell which can infect
PT host cell and form provirus
PS Example; Page 17; 28pp; English.
CC The universal retroviral vector pPOL15-R1 (given in Q76041) was
CC obtained by replacing the SV40 promoter and hpt gene of pPOL11-R1
CC (Q76038) with the multiple cloning site of pBluscript II KS+. The
CC vectors allow cell-type specific gene expression and eliminate risks
CC of downstream activation of cellular proto-oncogenes
Sequence 3878 BP; 922 A; 948 C; 988 G; 1070

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Query Match          72.2%  Score 417.4;  DB 1;  Length 3878;
Best Local Similarity 64.0%  Pred. No. 3,5e+126;
Matches 378;  Conservative 160;  Mismatches 31;  Indels 22;  Gaps 8

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   |||:|||||:||||:||||:||||:|||||:|||||:|||||:||||:||||:|
Db 684 GGGGCGCCGCGTCTCCACACTTCTTTGTGTGAGCTCGCGCCGCGAATTCGATTAATA 743
   ||:||||:||||:||||:||||:||||:|||||:|||||:|||||:||||:|

QY 58 aaguuuuuuucucuaauuucucagauuggcaguuagagagauuuuuuguguguuag 117
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Db	804	CTGTGCTACTGGTGGCGCAGAGGATCCGAGCTGATCCGTATCTTCGTGATCAAT	863
QY	177	uuuggggucucugccggau-uccucccaucggcagaagugcuaucuuuuu-----	228
Db	864	TTGGGGGCTGTCCGGGATACCTCCCCATCGCAGAGGTGCCAACTGCTTTTCGAAT	923
QY	229	--ucgaacuccggccgcgugaa-uaaagucuuuguuuguaucug-cgaagguuug	283
Db	924	TTCTCAACTCCGGCGCCGCTGAGTTAACTTGAATTTTGGTACCTGCCCAAGGCTTG	983
QY	284	ggagagucgga---gugggggagcugccgggaaguccaaccucgcucagcaggggac	340
Db	984	GGAGATCGGATGGTGGGGGAGACCTCCCGGGAAGCTCCACTCCGCTCAGACAGGGAC	1044
QY	341	gcccuagucugacucuguguaucugauuguuugugagccgucucgaagacguguaaa	400
Db	1044	GGCCCTGACCTGAGCTGTGTGATCTGATTTGTTTGAAGCCGTCCTTAAGAGGGGATA-	1107
QY	401	uaaagucuguuuguuuguuuguuuaaccuuguuuuuuucuaucuaucugacag	460
Db	1103	-CTAAGTGTGGCTTGTGTGTGTGTGTTCCTCTGTGTGTTCGTGCTGTTCGACAG	1161
QY	461	cgccucggaauugugugucacacacgcgcgcgucugcgaauaauaacuuagaauguu	520
Db	1162	CGCCTTGGGAATTTGTGTATCCACACCGCGGCGCTTGGAATATTACTTTGAGAACCTT	1221
QY	521	uuucucagugucucuguuuguaucuuucuuucuuucuuucuuucuuucgcggcg	571
Db	1222	TTGCTCCAGTGTTCCTGCTGTGATCTGCTCTCTCTCTCTCTCTCCCTCCGCGCG	1272

RESULT 5
 ID Q76040 standard; DNA; 5519 BP.
 DT 20-JUL-1995 (first entry)
 DE Retrovirus vector pPO11-R3.
 KW Cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
 KW long terminal repeat; LTR; encapsidation; gene transfer;
 KW gene therapy; ss.
 OS Spleen necrosis virus.
 PN M09429437-A.
 PD 22-DEC-1984.
 PF 07-JUN-1994; 006415.
 PR 07-JUN-1993; US-073345.
 PA (DYNB-) UNIV NEW JERSEY.
 PI Dornburg RC;
 DR WPI; 95-036467/05.
 PT Recombinant retrovirus vector; contg. non-retroviral gene, - has
 PT ability to produce progeny virus, in helper cell which can infect
 PT host cell and form provirus
 PS Example; Page 16-17; 28pp; English.
 CC New recombination-free, highly efficient retroviral vectors
 CC pPO11-R1 (given in Q76038), pPO11-R2 (Q76039) and pPO11-R3
 CC (Q76040) were obtained by replacing the U3 region of the left
 CC LTR of spleen necrosis virus with the IE promoter/enhancer of CMV,
 CC and extension of the encapsidation region. The vectors allow
 CC cell-type specific gene expression and eliminate risks of
 CC downstream activation of cellular proto-oncogenes.
 SQ Sequence 5519 BP; 1264 A; 1420 C; 1456 G; 1379 T;

	Query Match	70.9%	Score 410;	DB 1:	Length 5519;
	Best Local Similarity	62.9%	Pred. No. 1	le-123;	
	Matches 381;	Conservative 161;	Mismatches 50;	Indels 34;	Gaps 8
Oy	1	gggaguccgcucucacaca---	uuuuugagcgcgcgcgcacgaauuugaucguuaaa	57	

[illegible]

```

Query Match          70.9% Score 410. DB 1; Length 5525;
Best Local Similarity 62.9%; Pred. No. 1.1e-123; Indels 34; Gaps
Matches 381; Conservative 161; Mismatches 30;
QY      1 ggggucgcgcuguccacaca---uuugugagcgcgcgcgcgcagaauucgaucguanaa 57
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       681 GGAGTCGCCGCTCCACATTTGTCTGTGACGGCGGCAGATTGAATCTTGATATAA   740
QY      58 aaguuuuuuuuucauaauccuacagauuugcagugagagagauuuuugucuguguaq 117
         ||::::::::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       741 AATTTTTTTTTTCGAATCCTCAATTTGGAGTAGAGAGGATTTTCTGTGTTGTG 800
QY      118 gcugcccuacuggugugg--guagugucgcagcuanaucguauquauuacaaacu 176
         |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       801 CCTGGCTACTGGGTTGGCGCAGGATCCGAGCTGAATCCGTAGACTTCGTAACAAT 860
QY      177 uuggggucugucgcggaau-uucuccccaugcgaggaugucuaug-----n 224
         ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       861 TTGGGGGCTGTGTCGGGATACCCTCCCCTCCGAGAGGTGCCAACTCTTCTTCGAAT 920
QY      225 uuucugaacucgcgcgcgcguuag--uaaguaucuauuuuguuacucgcgcgaggguuq 283
         ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       921 TTTCTTCMACTCCGGGCGCGGTAGTTAGTACTTGATTTTGTGACTCGGAGGTTTG 980
QY      284 ggagagacgga----guagcggaacgcgcgcgcggaagaccuacucgcgcgcagagagac 340
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       961 GGAGGATCGGAGTAGTGTGGCGGAGACGCTGCCGGGAACTCCACTCCGCTCACAGGGGAC 1040
QY      341 gccucgacugagcuc-----uuuguaucguauuuguuugagucgcugucca 388
         ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1041 GCCCTGACCTGAGCTCAATTCAGATCTTGTGTACTGTATGTTGTTGAGCCGTCCHA 1100
QY      389 agacgcugaauaauaagucuguguuuuguuuguuuuguaucuuuguuuguc 448
         |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1101 AGACGCTATA--CTAGTGTGTGCTGTGTGTTGTTGTTGCTGTGTTGTTGCTG 1158
QY      449 acuuugcacgcgcgcgcgcgaauugugugcccacaacgcgcgcgcgcgcgaauaau 508
         ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1159 GTTTGTCCAGACGCGCTTGCGAATTTGGTACCAACACC CGCGCTTGGAATATACT 1218
QY      509 uugggaguuuuuuugccccacaguuucucguuuuguaucucucucucucucgcg 568
         ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db       1219 TTGGAGAGCCTTTTCCCTCCAGTGTCTTCGCTGTACTGCTCTCTCTCTCCG 1278
QY      569 ccgga 574
         |||||
Db       1279 CCGGA 1284

RESULT 7
ID      Q76038 standard; DNA; 5528 BP.
AC      Q76038;
DE      20-JUL-1995 (first entry)
DE      Retrovirus vector pPOII-R1.
KW      Retrovirus; vector; pPOII-R1; spleen necrosis virus; SNV;
KW      cytomegalovirus; CMV; intermediate-early promoter; IE promoter;
KW      long terminal repeat; LTR; encapsidation; gene transfer;
KW      gene therapy; SS.
OS      Spleen necrosis virus.
PN      MO9429437-A.
PD      22-DEC-1994.
PR      07-JUN-1994; US-073345.
PA      (UTNE-) UNIV NEW JERSEY.
PI      Dornburg RC.
PT      WPI; 95-036467/05.
PS      DR Recombinant retrovirus vector, contg. non-retroviral gene, - has
        ability to produce progeny virus, in helper cell which can infect
        host cell and form provirus
        Example; Page 13-14; 28pp; English.
```


[illegible]

13
 162572/c
 162572 standard; DNA; 2142 BP.
 27-OCT-1997 (first entry)
 Heat-resistant barley beta-amylase gene promoter containing DNA.
 Barley; heat resistant; promoter; genetic engineering; transgenic;
 plant; improved maturation; ds.
 Hordeum vulgare.
 MO9702353-A1.
 23-JAN-1997.
 05-JUL-1996.
 05-JUL-1995; JP-191028.
 (SAPB) SAPPORO BREWERIES.
 Ito K, Kinara M, Okada Y, Yoshigai N;
 WPI; 97-108966/10.
 Expression promoter for genes inserted into plant seeds - e.g.
 heat-resistant beta-amylase gene inserted into barley seeds
 Example 6: Page 20-21, 33pp; Japanese.
 T62572 is a DNA molecule comprising a heat resistant promoter derived
 from a barley beta-amylase (EC 3.2.1.2) gene and other sequences
 used for integration of this promoter into a reporter plasmid. The
 plasmid is used for the production of transgenic barley plants
 and seeds. Such plants and seeds have improved maturation properties.
 Sequence 2142 BP; 651 A; 487 C.
 105 maturation properties.

recombinant
express
Sequenc

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Tue Aug 8 08:33:20 2000

us-09-214-124-2-copy_265_578.rge

(1766) Page 1

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 10:53:39 ; Search time 4994.97 Seconds
(without alignments)
652.183 Million cell updates/sec

Title: US-09-214-124-2_COPY_265_578
314
Perfect score: 1 gnuaccucgcgagggguuuug.....ccucucgcgcggauggg 314
Sequence: 1 gnuaccucgcgagggguuuug.....ccucucgcgcggauggg 314

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 972840 seqs, 5187315402 residues

Total number of hits satisfying chosen parameters: 1945680

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba1:
2: gb_ba2:
3: gb_cm:
4: gb_cm:
5: gb_cm:
6: gb_cm:
7: gb_cm:
8: gb_cm:
9: gb_cm:
10: gb_cm:
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79: gb_cm:
80: gb_cm:
81: gb_cm:
82: gb_cm:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	314	100.0	578	5	A83549 Sequence 2
2	314	100.0	940	5	A83548 sequence 1
3	304.4	96.9	4292	82	AF006065 Fowlpox v
4	264.6	84.3	1530	81	RESNVX
5	149.4	47.0	891	81	REXX1
6	44.8	14.3	290	13	AU025522 Rattus no
7	37.6	12.0	378	13	AU026236 Rattus no
8	37.6	12.0	7218	5	I66494 Sequence 14
9	37.2	11.8	113440	55	AC020935 Homo sapi
10	37.2	11.8	70480	39	AC006973 Homo sapi
11	36.2	11.5	173618	57	AC019045 Homo sapi
12	36.2	11.5	2041	12	MUSEN2E1A
13	36.2	11.5	16832	42	AC014255
14	36.2	11.5	88866	41	AC010656
15	36.2	11.5	114958	51	AC008356 Drosophila
16	36.2	11.5	119182	51	AC008356 Drosophila
17	36.2	11.5	224230	34	AE003682 Drosophila
18	35.8	11.4	186518	60	AC016813 Homo sapi
19	35.4	11.3	72394	75	AC040913 Homo sapi
20	35.2	11.2	176043	77	AC027072 Homo sapi
21	35.2	11.2	213721	10	HS172820 Human DNA
22	35.2	11.1	155278	10	HS0655C4 Human DNA
23	34.8	11.1	168613	40	AL139318 Homo sapi
24	34.8	11.0	167656	31	AF001645 Homo sapi

Nature 285: 550-554
1980

PNAS 70 (4): 1230-
1234, 1982

	Query Match	47.68;	Score 149.4;	DB 81;	Length 891;	
	Best Local Similarity	64.0%;	Pred. No. 6.8e-35;			
	Matches 126;	Conservative 55;	Mismatches 11;	Indels 5;	Gaps 2;	
OY	1 guuacucgaggaagguaugugagaucgcga---guagcgagaccgucgcggagaucucca 57					
Ddb	697 GGTACTCTGCAGAGGTTTGGAGATCGAGATGGTGTCGGCGAGACGCTCCCGGAAGCTCCA 756					
OY	58 cuccgcacgaagcaggagagcccucgaucugacucucuguaucugauuuuguuagc 117					
Ddb	757 CCTCGGCTCAGACAGGGAGGCCCTGGCTGAGCTGTGGTAATCATGTGTGTGTGAGCC 816					
OY	118 guuccaagagcgguguaauaaucugucguguauguuuguuuuuacucuuugnu 177					
Db	817 GTCCCTAAACCGCTGAATA--CTAAGTCGTGGCTGTGTGTGTGTGTGTGTGTGT 874					
OY	178 guucgucacuuugucac 194					
Db	875 GTTCGTCGTTTGTGCGAC 891					
RESULT	6					
AU025522						
LOCUS	AU025522 290 bp DNA STS 02-MAR-1999					
DEFINITION	Rattus norvegicus; OTSUKA clone, OT29.32/731C09, microsatellite sequence, tagged site.					
ACCESSION	AU025522					
VERSION	AU025522.1 GI:4515445					
KEYWORDS	STS.					
SOURCE	Rattus norvegicus DNA, clone:OT29.32/731C09.					
ORGANISM	Rattus norvegicus Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Sciurognathi; Muridae; Murinae; Rattus. Eurharia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
REFERENCE	1 (sites)					
AUTHORS	Watanabe,T.K., Hishigaki,H., Kanemoto,N., Miyakita,Mizoguchi,A., Oga,K., Okuno,S., Ono,T., Tsuji,A., Hayashi,H., Adachi,M., Yamasaki,Y., Iriye,Y., Takahashi,E., Takagi,T., Nakamura,Y. and Tanigami,A.					
TITLE	The large-scale mapping of rat microsatellite markers					
JOURNAL	Unpublished (1998)					
REFERENCE	2 (bases 1 to 290)					

RESULT	9
AC020935	
LOCUS	
DEFINITION	AC020935 113440 bp DNA HTG
SEQUENCE	Homo sapiens chromosome 5 clone CTD-2280P20, WORKING DRAFT
ACCESSION	AC020935
VERSION	AC020935.2 GI:6957623
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
AUTHORS	Eutheria; Primates; Catarrhini; Homidae; Homo. DOE Joint Genome Institute.

MAPPING INFORMATION: The sequence of this clone was established apart of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), Johns Hopkins University, and the Washington Department of Genetics (Washington University) and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIG/CH7>, send

Db 19737 ATTGATGTTGCTCTGACTATG 19713

RESULT 11

LOCUS AC019045

DEFINITION Homo sapiens chromosome UL clone RP11-63G23, WORKING DRAFT

ACCESSION AC019045

VERSION AC019045.4 GI:7230851

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Waterston,R.H..

TITLE The sequence of Homo sapiens clone

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 173618)

AUTHORS Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108 USA

COMMENT On Mar 13, 2000 this sequence version replaced gi:7021777.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: http://genome.wustl.edu/gsc/index.shtml

----- Project Information -----

Center project name: H_NH0063G23

----- Summary Statistics -----

Sequencing vector: M13; 88%

Sequencing vector: plasmid; 12%

Chemistry: Dye-terminator Big Dye; 12% of reads

Chemistry: Dye-terminator Big Dye; 12% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 16386 bases at least Q40

Consensus quality: 167019 bases at least Q30

Consensus quality: 168966 bases at least Q20

Insert size: 192000; agarose-fp

Insert size: 171918; sum-of-coverage

Quality coverage: 3.64 in Q20 bases; sum-of-coverage

Quality coverage: 4.09 in Q20 bases; sum-of-coverage

----- NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. -----

1 1455: contig of 1455 bp in length

1456 1555: gap of unknown length

1556 4255: contig of 2700 bp in length

4256 4355: gap of unknown length

4356 7303: contig of 2947 bp in length

7303 7403: gap of unknown length

7403 10141: contig of 2739 bp in length

10141 10241: gap of unknown length

10241 16585: contig of 6344 bp in length

16585 16686: gap of unknown length

16686 21874: contig of 5189 bp in length

21874 21974: gap of unknown length

21974 27791: gap of 5817 bp in length

27791 27891: gap of unknown length

27891 34069: contig of 6178 bp in length

34069 34170: gap of unknown length

34170 39365: contig of 5196 bp in length

39365 39366: gap of unknown length

39466 45870: contig of 6405 bp in length

45871 45970: gap of unknown length

45971 54439: contig of 8469 bp in length

54439 54538: gap of unknown length

54538 63883: contig of 9344 bp in length

63883 63983: gap of unknown length

63983 73653: contig of 9670 bp in length

73653 73754: gap of unknown length

73754 83831: contig of 10077 bp in length

83831 83930: gap of unknown length

83930 83931: gap of 15459 bp in length

83931 99390: gap of unknown length

99390 99489: gap of unknown length

99489 113715: contig of 14226 bp in length

113715 113815: gap of unknown length

113815 139051: contig of 25236 bp in length

139051 139151: gap of unknown length

139151 173618: contig of 34467 bp in length.

----- Location/Qualifiers -----

1. 173618

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="UL"

/clone="RP11-63G23"

BASE COUNT 57346 a 30229 c 30623 g 53714 t 1706 others

ORIGIN

Query Match 11.8%; Score 37; DB 57; Length 173618;

Best Local Similarity 26.6%; Pred. No. 1.3;

Matches 29; Conservative 35; Mismatches 45; Indels 0; Gaps 0;

QY 78 ccuagucugagucugucugucugucugucugucugucugucugucac 137

Db 111333 CCATTAACCCCGTTGACCTTAAGAGCGTGTGTTATATATATGAGAGAT 111392

QY 138 auaagucugugugugugugugugugugucugucugucac 186

Db 111393 TTCCACGATGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGACAC 111441

RESULT 12

MUSENZEIA 2041 bp DNA ROD 27-APR-1993

LOCUS M88481

DEFINITION Mouse enzyme E1 (E1) pseudogene, complete cds.

ACCESSION M88481.1 GI:193034

VERSION M88481.1 GI:193034

KEYWORDS enzyme E1; pseudogene.

SOURCE Mus musculus (strain 163H) male DNA.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 2041)

AUTHORS Mitchell,M.J., Woods,D.R., Tucker,P.K., Opp,J.S. and Bishop,C.E.

TITLE Homology of a candidate spermatogenic gene from the mouse Y chromosome to ubiquitin-activating enzyme E1

JOURNAL Nature 354, 483-486 (1991)

MEDLINE 92086048

REFERENCE 2 (bases 1 to 2041)

AUTHORS Tucker,P.K., Phillips,K.S. and Lundrigan,B.

TITLE A mouse Y chromosome pseudogene is related to human ubiquitin activating enzyme E1

JOURNAL Mamm. Genome (1992) In press

FEATURES

source

1. 2041

/organism="Mus musculus"

/strain="163H"

/db_xref="taxon:10090"

/sex="male"

/join(372..443,680..877,1438..1512,1617..1799)

gene

372..443

/gene="E1"

exon

/note="putative"

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/citation={2}
/number=1
join(372, .443,680, .877,1438,
/gene="E1"
.1512,1617, .1799)

```

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        /product="enzyme E1"
        680. .877
    exon

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exon	number
1	1438..1512

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/note="putative"
/citation=[2]
/number=3
1617. .1799
exon

```

BASE COUNT	448 a	463 c	494 g	636 t
ORIGIN	chromosome Y.			

Query Match	11.5%	Score	36.2;	DB	12;	Length	2041;
Best Local Similarity	27.6%	Pred. No.	1.8;				
Matches	29;	Conservative	33;	Mismatches	43;		

Dy 91 ucuguguaucugauuguuugagccgucuccaaagcgguguaauaanaagucugugu 150
::: :||:|::|:
Db 249 TCCTTACTACAGGTTGTCTCATAATGTATCAAGAAGGGTTTTTGCGGTGTCTGTT 308

Db
309 GTTGTTCGTTGTTTGTTCGTTGGCTATTGCTGACA 353

RESULT	13
AC014255/c	
LOCUS	
DEFINITION	AC014255 16832 bp DNA
DESCRIPTION	Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, In ordered
ACCESSION	AC014255
VERSION	AC014255.1 GI:6437080
KEYWORDS	HTG; HTGS_PHASE2.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster

REFERENCE

1 (bases 1 to 16832)

Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

JOURNAL COMMENT
Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CNV.10331400 by the Celera Genomics database.

- * NOTE: This is a 'working draft' sequence.
- * This sequence will be replaced
- * by the finished sequence as soon as it is available and
- * the accession number will be provided

FEATURES	Location/Qualifiers
source	1. 16832
BASE COUNT	/organism="Drosophila melanogaster" /db_xref="taxon:7227"
ORIGIN	5004 a 3392 c 3347 g 5089 t

Query Match	11.58;	Score 36;	DB 42;	Length 16832;
-------------	--------	-----------	--------	---------------

Best Local Similarity	31.5%	Pred. No. 2.3
Matches	29; Conservative	28; Mismatches
	35; Indels	0; Gaps
		0

D5 8440 CTTGTGTTGTTTGCCGGCACACAAAGTGCATAAATTAAATGCTGTGTGGGTGCTGTTTG 838

Db 8380 TTTGTTGCTGCCTTTTGTCGCTTGTAGTGG 8349

RESULT	14
LOCUS	AC010696
DEFINITION	AC010696 88866 bp DNA HTG 16-OCT-1999
ACCESSION	Drosophila melanogaster clone RC18-154P, ** SEQUENCING IN
VERSION	AC010696 ** 69 unordered pieces.
KEYWORDS	AC010696.2 GI:5917940
SOURCE	HTG: HTGS_PHASE1.
ORIGIN	fruit fly.

REFERENCE
AUTHORS

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 88866)
Muzny, D.M., Adams, C., Bailey, M., Barbara, I. Plankenburg, W.

Burrell, C., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,
Burrell, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Donah-Rashid, N.,
Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
Forcum-Tansey, J., Frantz, P., Ganesha, R., Gorrell, J.H., Gorrell, L.L.,
Guevarra, M., Harris, K., Hernandez, J., Hodgson, A., Hogue, M.,
Holloway, C., Hosack, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M.,
Kell, S., Kondziejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R.,
Martin, R., Martinez, C., McLeod, M.P., Mel, G., Morgan, M., Morris, S.,
Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G.,
Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.L., Quiles, M.,
Reller, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E.,
Shen, H., Simon, M., Sparks, A., Stamps, A., Sugrue, R., Taber, P.,
Taylor, I., Vasquez, L., Vinson, R., Vo, O., Wabwah, M., Wellington, S.,
Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J.,
Wrenstorf, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, R.

TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 88866)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (18-SEP-1999)
COMMENT	Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
	On Sep 22, 1999 this sequence version replaced 015000007

* NOTE: runs is a working draft sequence. It currently
* consists of 69 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1
 * 853: contig of 852 bp in length
 * 1684
 * 1684: contig of 831 bp in length
 * 2543
 * 3512: contig of 859 bp in length
 * 3917
 * 5228: contig of 1374 bp in length
 * 5229
 * 5448: contig of 1312 bp in length
 * 6449
 * 7285: contig of 1220 bp in length
 * 7286
 * 7285: contig of 837 bp in length
 * 8166
 * 8166: contig of 978 bp in length
 * 9101
 * 10441: contig of 937 bp in length
 * 10442
 * 10441: contig of 1341 bp in length
 * 11653
 * 11652: contig of 1211 bp in length
 * 12386: contig of 734 bp in length

*	7460	7539:	gap of unknown length
*	7540	8334:	contig of 795 bp in length
*	8335	8414:	gap of unknown length
*	8415	9145:	contig of 751 bp in length
*	9166	9245:	gap of unknown length
*	9246	9884:	contig of 639 bp in length
*	9885	9964:	gap of unknown length
*	9965	11112:	contig of 1148 bp in length
*	11113	11192:	gap of unknown length
*	11296	12395:	contig of 1203 bp in length
*	12396	12475:	gap of unknown length
*	12476	13349:	contig of 1074 bp in length
*	13350	13529:	gap of unknown length
*	13630	14949:	contig of 1330 bp in length
*	14950	15029:	gap of unknown length
*	15030	16127:	contig of 1098 bp in length
*	16128	16207:	gap of unknown length
*	16208	17350:	contig of 1143 bp in length
*	17351	17431:	gap of unknown length
*	19082	19081:	contig of 1651 bp in length
*	19162	20834:	contig of 1673 bp in length
*	20835	20913:	gap of unknown length
*	20915	21896:	contig of 984 bp in length
*	21899	21978:	gap of unknown length
*	21979	22671:	contig of 653 bp in length
*	22672	22751:	gap of unknown length
*	22752	23766:	contig of 1013 bp in length
*	23765	24974:	gap of unknown length
*	23845	25053:	contig of 1129 bp in length
*	24974	25780:	contig of 727 bp in length
*	25054	25860:	gap of unknown length
*	25781	27141:	contig of 1281 bp in length
*	25861	27221:	gap of unknown length
*	27142	28275:	contig of 1054 bp in length
*	27222	28355:	gap of unknown length
*	28275	30242:	contig of 1887 bp in length
*	28356	30322:	gap of unknown length
*	30243	31945:	contig of 1623 bp in length
*	30323	32025:	gap of unknown length
*	31946	32928:	contig of 903 bp in length
*	32026	33008:	gap of unknown length
*	33029	35085:	contig of 2077 bp in length
*	35086	35165:	gap of unknown length
*	35166	36633:	contig of 1468 bp in length
*	36634	36713:	gap of unknown length
*	36714	38597:	contig of 1884 bp in length
*	38598	41039:	gap of unknown length
*	38677	41039:	contig of 2352 bp in length
*	41040	41119:	gap of unknown length
*	41120	42801:	contig of 1662 bp in length
*	42802	44281:	gap of unknown length
*	42882	44451:	contig of 1570 bp in length
*	44452	46258:	gap of unknown length
*	44532	46358:	contig of 1727 bp in length
*	46259	46358:	gap of unknown length
*	46359	47721:	contig of 1883 bp in length
*	47722	50320:	gap of unknown length
*	47802	50320:	contig of 2419 bp in length
*	50231	51504:	gap of unknown length
*	50301	51505:	contig of 1204 bp in length
*	51505	51584:	gap of unknown length
*	51585	52896:	contig of 1312 bp in length
*	52897	52976:	gap of unknown length
*	52977	55033:	contig of 2059 bp in length
*	55036	55115:	gap of unknown length
*	55116	57120:	contig of 2005 bp in length
*	57121	57200:	gap of unknown length
*	57201	59206:	contig of 2006 bp in length
*	59207	59286:	gap of unknown length
*	59287	61708:	contig of 2422 bp in length
*	61709	61786:	gap of unknown length

*	61789	63710: contig of 1922 bp in length
*	63711	63750: gap of unknown length
*	63791	65200: contig of 1410 bp in length
*	65201	65280: gap of unknown length
*	65281	67585: contig of 2305 bp in length
*	67585	67665: gap of unknown length
*	67666	70390: contig of 2725 bp in length
*	70391	70470: gap of unknown length
*	70471	72950: contig of 2480 bp in length
*	72951	73030: gap of unknown length
*	73031	76068: contig of 3038 bp in length
*	76069	76148: gap of unknown length
*	76149	80201: contig of 4053 bp in length
*	80202	80281: gap of unknown length
*	80282	88995: contig of 8714 bp in length
*	88996	89075: gap of unknown length
*	89076	89766: contig of 691 bp in length
*	89767	89846: gap of unknown length
*	88847	90501: contig of 655 bp in length
*	90502	90581: gap of unknown length
*	90582	91197: contig of 616 bp in length
*	91198	91277: gap of unknown length
*	91278	91882: contig of 605 bp in length
*	91883	91963: gap of unknown length
*	91963	92559: contig of 597 bp in length
*	92560	92639: gap of unknown length
*	92640	93335: contig of 696 bp in length
*	93336	93415: gap of unknown length
*	93416	94074: contig of 659 bp in length
*	94075	94154: gap of unknown length
*	94155	94793: contig of 639 bp in length
*	94794	94873: gap of unknown length
*	94874	95491: contig of 618 bp in length
*	95492	95571: gap of unknown length
*	95572	96257: contig of 686 bp in length
*	96258	96337: gap of unknown length
*	96338	96916: contig of 579 bp in length
*	96917	96996: gap of unknown length
*	96997	97645: contig of 649 bp in length
*	97646	97725: gap of unknown length
*	97726	98402: contig of 677 bp in length
*	98403	98482: gap of unknown length
*	98483	99131: contig of 649 bp in length
*	99132	99211: gap of unknown length
*	99212	99806: contig of 595 bp in length
*	99807	99886: gap of unknown length
*	99887	100488: contig of 602 bp in length
*	100489	100568: gap of unknown length
*	100569	101206: contig of 638 bp in length
*	101207	101286: gap of unknown length
*	101287	101991: contig of 705 bp in length
*	101992	102071: gap of unknown length
*	102072	102681: contig of 610 bp in length
*	102682	102761: gap of unknown length
*	102762	103386: contig of 625 bp in length
*	103387	103466: gap of unknown length
*	103467	104106: contig of 640 bp in length
*	104107	104186: gap of unknown length
*	104187	104842: contig of 656 bp in length
*	104843	104922: gap of unknown length
*	104923	105606: contig of 664 bp in length
*	105607	105686: gap of unknown length

Query Match	11.5%	Score 36;	DB 51;	Length 114958;
Best Local Similarity	31.5%	Pred. No. 2.5;		
Matches	29;	Conservative	28;	Mismatches 35; Indels 0; Gaps 0;
QY 101	cugaugugugugcagccgucucacagcggugauaauaagucugugugugugugug 160			
Db 57736	CTTGCTGTTGTTTCGCCGCACACAAGTGTCAATTAATTAATGCTGCTGGTGTGTTG 57677			
QY 161	uuuguaacuguguuugucucacugucug 192			

Tue Aug 8 08:33:20 2000

us-09-214-124-2_copy-265_578.rge

Page 12

DB 57676 TTTGTTGCTGCTTTTGTGCTTGTAGTGG 57645

Search completed: August 7, 2000, 10:55:16
Job time: 6090 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 09:28:43 ; Search time 172.61 Seconds
(without alignments)
250,232 Million cell updates/sec

Title: US-09-214-124-2_COPY_265_578

Sequence: 1 gguacucgcggaggguuug.....ccuucucgcggaggg 314

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 243080 seqs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_NA.*

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3: /cgn2-6/ptodata/1/lna/5C.COMB.seq:*
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6: /cgn2-6/ptodata/1/lna/PTCUS.COMB.seq:*
7: /cgn2-6/ptodata/1/lna/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37.6	12.0	7218	1 US-08-232-463-14	Sequence 14, Appl
2	30.6	9.7	1276	4 US-08-793-599-1	Sequence 1, Appl
3	30.6	9.7	2142	4 US-08-793-599-3	Sequence 3, Appl
4	28.8	9.2	3934	5 US-09-226-568-18	Sequence 18, Appl
5	28.8	9.2	3946	1 US-08-077-848A-1	Sequence 1, Appl
6	28.8	9.2	3946	5 US-09-211-640-1	Sequence 1, Appl
7	28.8	9.2	3946	6 PCT-US94-03547-1	Sequence 1, Appl
8	28.8	9.2	11531	1 US-08-068-945A-1	Sequence 1, Appl
9	28.8	9.2	11531	2 US-08-442-806-1	Sequence 1, Appl
10	28.2	9.0	221	1 US-08-222-177A-17	Sequence 17, Appl
11	28.2	9.0	278	1 US-08-222-177A-17	Sequence 17, Appl
12	28	8.9	3240	2 US-08-162-081B-34	Sequence 34, Appl
13	28	8.9	3240	3 US-08-162-081B-34	Sequence 34, Appl
14	28	8.9	3412	2 US-08-780-872-32	Sequence 32, Appl
15	28	8.9	3412	3 US-08-162-081B-32	Sequence 32, Appl
16	27.6	8.8	8224	4 US-08-780-872-32	Sequence 32, Appl
17	27.6	8.8	8224	4 US-08-780-872-32	Sequence 32, Appl
18	27.2	8.7	2277	2 US-08-676-974-2	Sequence 2, Appl
19	27.2	8.7	2277	2 US-08-676-974-2	Sequence 2, Appl
20	27.2	8.7	2277	4 US-09-098-487-2	Sequence 11, Appl
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22	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
23	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
24	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
25	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
26	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
27	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
28	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
29	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
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39	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
40	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
41	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
42	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
43	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
44	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl
45	27.2	8.7	2277	4 US-08-781-802-11	Sequence 9, Appl

27	27	8.6	2488	2 US-08-279-270A-2	Sequence 2, Appl
28	26.8	8.5	20235	2 US-07-642-734C-3	Sequence 3, Appl
29	26.2	8.3	1155	5 US-08-860-368B-19	Sequence 19, Appl
30	26.2	8.3	2381	3 US-08-484-993B-9	Sequence 9, Appl
31	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
32	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
33	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
34	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
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37	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
38	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
39	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
40	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
41	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
42	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
43	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
44	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl
45	26.2	8.3	2381	4 US-08-484-993B-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)836-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMEDIATE SOURCE:
CLONE: pTZgpt-F15
US-08-232-463-14

us-09-214-124-2_copy_265_578.rn

Query Match	12.0%;	Score 37.6;	DB 1;	Length 7218;
Best Local Similarity	4.5%;	Pred. No. 0.0073;		
Matches 13;	Conservative 156;	Mismatches 117;	Indels 0;	Gaps 0;

RESULT 2
US-08-793-599-1/c
: Sequence 1, Application US/08793599

Query Match	9.73;	Score 30.6;	DB 4;	Length 1276;
Best Local Similarity	27.18;	Pred No. 0.67;		
Matches 23;	Conservative	28;	Mismatches 34;	Indels 0;
			Gaps	0.

RESULT 3
US-08-793-599-3/c
: Sequence 3, Application US/08793599

RESULT 3
US-08-793-599-3/c
; Sequence 3, Application US/0/
; Patent No. 5952489
; GENERAL INFORMATION:
; APPLICANT: OKADA, YUKIO
; APPLICANT: YOSHIGI, NAOHIRO
; APPLICANT: ITO, KAZUTOSHI

Query Match	9.7%;	Score 30.6;	DB 4;	Length 2142;
Best Local Similarity	27.1%;	Pred. No. 0.84;		
Matches	23;	Conservative	28;	Mismatches 34; Indels 0; Gaps 0.

RESULT 4
US-09-226-568-18/c
; Sequence 18, Application US/09226568

Query Match	9.2%	Score 28.8	DB 5	Length 3934
Best Local Similarity	56.2%	Pred No 4.3		
Matches 27	Conservative	9	Mismatches	12
			Indels	0
			Gaps	0

RESULT 5
US-08-077-848A-1/c
; Sequence 1, Application US/08077848A

RESULT 5
US-08-077-848A-1/c
Sequence 1, Application US/08077848A
Patent No. 5470955
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1

QY 41 gcugccgggaagcuccaccuccgucagcaggagagcccccugaucugagucuguguan 100
Db 7107 GCTCACTGCAACCTCCTCCTGCTCAAGTATCTCTGACCAACCTCCCATGTAG 7166
QY 101 cugauugugugagcgcugcuccagagcagugauauaagucuguguguguguguan 160
Db 7167 CTGGAGCTACAGCCATGCTCCATGCTCCAGATATTTTCTGTGTGTAGAGGAT 7226
QY 161 uugugacugugugugugugucagucugucug 192
Db 7227 GGAGTTTATGCTGTAGCTAGATGATCTCG 7258

RESULT 9
US-08-442-806-1
Sequence 1, Application US/08442806
Patent No. 5716817

GENERAL INFORMATION:
APPLICANT: Bjursell, Gunnar
APPLICANT: Carlsson, Peter
APPLICANT: Enerback, Sven
APPLICANT: Hansson, Lennart
APPLICANT: Lidberg, Ulf
APPLICANT: Nilsson, Jeanette
TITLE OF INVENTION: Genomic DNA Sequences
TITLE OF INVENTION: Encoding Human BSSL/CEL
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: White & Case
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2787

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,806
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/068,945
FILING DATE: 27-MAY-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
APPLICATION DATA:
APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
APPLICATION DATA:
APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Steiner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)819-8783
TELEFAX: (212)354-8113

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
FEATURE:
NAME/KEY: CDS
LOCATION: join(1653..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11391)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: join(1722..1727, 4071..4221, 4307..4429, 4707
LOCATION: ..4904, 6193..6323, 6501..6608, 6751..6868, 8335
LOCATION: ..8521, 8719..8922, 10124..10321, 10650..11391)
OTHER INFORMATION: /EC number=3.1.1.1
FEATURE:
NAME/KEY: 5'UTR
LOCATION: 1..1640
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 1611..1617
FEATURE:
NAME/KEY: exon
LOCATION: 1641..1727
FEATURE:
NAME/KEY: exon
LOCATION: 4071..4221
FEATURE:
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LOCATION: 4307..4429
FEATURE:
NAME/KEY: exon
LOCATION: 4707..4904
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NAME/KEY: exon
LOCATION: 6193..6323
FEATURE:
NAME/KEY: exon
LOCATION: 6501..6608
FEATURE:
NAME/KEY: exon
LOCATION: 6751..6868
FEATURE:
NAME/KEY: exon
LOCATION: 8335..8521
FEATURE:
NAME/KEY: exon
LOCATION: 8719..8922
FEATURE:
NAME/KEY: exon
LOCATION: 10124..10321
FEATURE:
NAME/KEY: exon
LOCATION: 10650..11490
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 11491..11531

US-08-442-806-1

Query Match 9.28; Score 28.8; DB 2; Length 11531;
Best Local Similarity 33.68; Pred. No. 6.9;
Matches 51; Conservative 24; Mismatches 77; Indels 0; Gaps 0;

QY 41 gcugccgggaagcuccaccuccgucagcaggagagcccccugaucugagucuguguan 100
Db 7107 GCTCACTGCAACCTCCTCCTGCTCAAGTATCTCTGACCAACCTCCCATGTAG 7166
QY 101 cugauugugugagcgcugcuccagagcagugauauaagucuguguguguguguan 160
Db 7167 CTGGAGCTACAGCCATGCTCCATGCTCCAGATATTTTCTGTGTGTAGAGGAT 7226

NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE: Caucasian
TISSUE TYPE: Blood
IMMEDIATE SOURCE:
CLONE: Mfd154
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 5q
FEATURE:
NAME/KEY: repeat_region
LOCATION: 76..118
OTHER INFORMATION: /rpt_type= "tandem"
OTHER INFORMATION: /rpt_family= "(dc-da)n.(dc-dt)n"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 20..39
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
FEATURE:
NAME/KEY: misc_feature
LOCATION: complement (198..217)
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..278
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "Only one strand sequenced"
PUBLICATION INFORMATION:
AUTHORS: Weber, J. L.
AUTHORS: Polymeropoulos, M. H.
AUTHORS: May, P. E.
AUTHORS: Kwitek, A. E.
AUTHORS: Xiao, H.
AUTHORS: McPherson, J. D.
AUTHORS: Wasmuth, J. J.
TITLE: Mapping of human chromosome 5 microsatellite
TITLE: polymorphisms
JOURNAL: Genomics
DATE: 1991
PUBLICATION INFORMATION:
AUTHORS: Weber, James L.
AUTHORS: May, Paula E.
TITLE: Abundant Class of Human DNA Polymorphisms
TITLE: Which Can Be Typed Using the Polymerase Chain
JOURNAL: Am. J. Hum. Genet.
VOLUME: 44
PAGES: 388-396
DATE: 1989
US-08-222-177A-52

Query Match 9.9%: Score 28.2; DB 1; Length 278;
Best Local Similarity 30.5%: Pred. No. 2.1;
Matches 32; Conservative 25; Mismatches 48; Indels 0; Gaps 0;
QY 79 ccgagucugagcucuguguaucugugugagccugucuccaagaagcguguaa 138
DB 4 CCATTCTGGGGCACATGATCTATCCATGATGACACAGCCGGGAAGCTCTGTGTG 63
QY 139 uagucuguguguguguguguguaucugugugugugugugugugugug 183
DB 64 AAATCTGAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 108
RESULT 12
US-08-162-081B-34
Sequence 34, Application US/08162081B
Patent No. 5824492
GENERAL INFORMATION:
APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter
APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: IUD 5256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-162-081B-34
Query Match 8.9%: Score 28; DB 2; Length 3240;
Best Local Similarity 34.2%: Pred. No. 7.2;
Matches 26; Conservative 20; Mismatches 30; Indels 0; Gaps 0;
QY 140 aagucuguguguguguguguaucugugugugugugugugagcagcagc 199
DB 2475 AAATCAAGCTCTGATCTTCGAATGCTTATGCTGTGTGTGTGTGTGTGTGT 2534
QY 200 ccugcgaugugugug 215
DB 2535 GGGACTTATTCAGGTG 2550

Tue Aug 8 08:33:21 2000

us-09-214-124-2_copy_265_578.rn1

Page 9

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1 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
2 COMPUTER: IBM PS/2
3 OPERATING SYSTEM: PC-DOS
4 SOFTWARE: Wordperfect
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/780,872
7 FILING DATE: 09-JAN-1997
8 CLASSIFICATION: 435
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 08/162,081
11 FILING DATE: February 7, 1994
12 APPLICATION NUMBER: PCT/GB93/00761
13 FILING DATE: 13 April 1993
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Pasqualini, Patricia A.
16 REGISTRATION NUMBER: 34,894
17 REFERENCE/DOCKET NUMBER: LUD 5256
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: (212) 688-9200
20 TELEFAX: (212) 838-3884
21 INFORMATION FOR SEQ ID NO: 32:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 3412 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single or double
26 TOPOLOGY: linear
27 FEATURE:
28 NAME/KEY: CDS
29 LOCATION: 1..3204
30 OTHER INFORMATION: /standard_name= "CDS"
31
32 US-08-780-872-32

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Query Match	8.9%	Score 26	DB 3	Length 3412
Best Local Similarity	34.2%	Pred. No. 7.4		
Matches	26	Conservative	20	Mismatches 30; Indels 0; Gaps 0
Qy	140	aaaguguguuuguguuuguuuuuacacuguguuuguuugucacuuugucagacagcgc	199	
Db	2475	AAATCAGCTCTGTAATCTGAAATGTTACTTATGCTGTCTGTCATTCGTGACGTGT	2534	
Qy	200	ccugcgaaauugugug	215	
Db	2535	GGGACTTAATGAGGTG	2550	

Search completed: August 7, 2000, 09:28:54
Job time: 908 sec

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C	33	27.2	8.7	2277	1	V13834
---	----	------	-----	------	---	--------

[illegible]

ALIGNMENTS

34	27.2	8.7	2442	1	X15602	<i>Enterococcus faecalis</i>
35	27.2	8.7	2643	1	V71207	DNA encoding enter
C 36	27.2	8.7	3513	1	V71202	DNA encoding enter
C 37	27.2	8.7	4315	1	T87501	DNA encoding therm
C 38	27.2	8.7	11288	1	G90512	CEA Clone HindIII
C 39	27.2	8.7	15036	1	V55267	<i>Carthoembryonic a</i>
C 40	27	8.6	1830	1	V35772	<i>Klebsiella pneumoniae</i>
41	27	8.6	2281	1	Q47834	Murine interleukin
42	27	8.6	2487	1	Q45332	Human epidermal su
C 43	27	8.6	2468	1	T95887	DNA for epidermal
C 44	27	8.6	4746	1	T47874	<i>K. pneumoniae</i> diol
C 45	27	8.6	11832	1	V27148	<i>Nucleotide sequen</i>

PA (UYNE-) UNIT NEW JERSEY.
 PI Dornburg RC:
 DR WPI: 95-036467/05.
 PT Recombinant retrovirus vector, contg. non-retroviral gene, - has
 PT ability to produce progeny virus, in helper cell which can infect
 PS host cell and form provirus
 Example: Page 17: 28pp: English.
 CC The universal retroviral vector pPOL15-R1 (given in 076041) was
 CC obtained by replacing the SV40 promoter and hpt gene of pPOL11-R1
 CC (076038) with the multiple cloning site of pBluescript II KS. The
 CC vectors allow cell-type specific gene expression and eliminate risks
 CC of downstream activation of cellular proto-oncogenes.
 SQ Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T;

Query Match Best Local Similarity 79.2%; Score 248.6; DB 1; Length 3878;
 Matches 198; Conservative 84; Mismatches 14; Indels 5; Gaps 2;

OY 10 cgaaggguuugggaggaucgga---guugcgggagcgucggcggaagcuccacuccguc 66
 DB 974 CGAGGGGTTGGAGAGATCGAGTGTGGCGGAGCGTGGCGGAGACTCCACCTCCGCTC 1033
 OY 67 agcaggggagcgcccgagcucgagcucgucgucgucgucgucgucgucgucgucguc 126
 DB 1034 AGCAGGGGAGCGCCCTGACCTGCTGTGATCTGATCTGTGTGAGCGCTCCCTAAG 1093
 OY 127 acgguuauauaauagucgucgucgucgucgucgucgucgucgucgucgucgucguc 186
 DB 1094 ACGGTGATTA--CTAAGTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1151
 OY 187 ungucgacagcgcccgagcucgucgucgucgucgucgucgucgucgucgucgucguc 246
 DB 1152 TGTGTGACAGCGCCCTGCGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1211
 OY 247 ggaaggucuuuugcgucgucgucgucgucgucgucgucgucgucgucgucgucguc 306
 DB 1212 GGAGAGCCTTTGCTTCCCTGCTGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1271
 OY 307 g 307
 DB 1272 G 1272

RESULT 5
 076040
 ID 076040 standard; DNA; 5519 BP.
 AC 076040;
 DE 20-JUL-1995 (first entry).
 DR Retrovirus vector pPOL11-R3.
 KW Retrovirus; vector; pPOL11-R3; spleen necrosis virus; SNV;
 KW cytomagalovirus; CMV; intermediate-early promoter; IE promoter;
 KW long terminal repeat; LTR; encapsidation; gene transfer;
 OS Spleen necrosis virus.
 PN W09429437-A.
 PD 22-DEC-1994.
 PE 07-JUN-1994; U06415.
 PR 07-JUN-1993; US-073345.
 PA (UYNE-) UNIT NEW JERSEY.
 PI Dornburg RC:
 DR WPI: 95-036467/05.
 PT Recombinant retrovirus vector, contg. non-retroviral gene, - has
 PT ability to produce progeny virus, in helper cell which can infect
 PS host cell and form provirus
 Example: Page 16-17: 28pp: English.
 CC New recombination-free, highly efficient retroviral vectors
 CC pPOL11-R1 (given in 076038), pPOL11-R2 (076039) and pPOL11-R3
 CC (076040) were obtained by replacing the U3 region of the left
 CC LTR of spleen necrosis virus with the IE promoter/enhancer of CMV,
 CC and extension of the encapsidation region. The vectors allow
 CC cell-type specific gene expression and eliminate risks of
 CC downstream activation of cellular proto-oncogenes.

SQ Sequence 5519 BP; 1264 A; 1420 C; 1456 G; 1379 T;

Query Match Best Local Similarity 76.0%; Score 238.6; DB 1; Length 5519;
 Matches 208; Conservative 86; Mismatches 14; Indels 17; Gaps 3;

OY 1 gnuaccucgagggguuugggaggaucgga---guugcgggagcgucggcggaagcucca 57
 DB 956 GGTACCTCCGAGAGGTTTGGAGAGATCGAGTGTGGCGGAGCTCCGGAGAGCTCCA 1015
 OY 58 ccucgcgucagagggagggagcccgucgagcuc-----uguggaucugau 105
 DB 1016 CTTCCCTCAGCAGGGGAGCGCCCTGACCTGACCTGCAATTCAGATCTTGTGATCTGAT 1075
 OY 106 uguuugugagccgucgucgucgucgucgucgucgucgucgucgucgucgucguc 165
 DB 1076 TGTGTGTGAGCGCTGCTCCCTAGACGCTGATA--CTAAGTCTGTGCTGTGTGTGTGT 1133
 OY 166 uaccuuguuuugcucgucgucgucgucgucgucgucgucgucgucgucgucguc 225
 DB 1134 TCCCTGT 1193
 OY 226 gggcucgucgagaaauagucgucgucgucgucgucgucgucgucgucgucgucguc 285
 DB 1194 GCGCTTCGAAATATATTCTTTGGAGAGCTTTTGTCTCAGTCTCTCTCTCTCTCTCT 1253
 OY 286 uccucucucucucucgucgucgucgucgucgucgucgucgucgucgucgucguc 310
 DB 1254 TCCCT 1278

RESULT 6
 076039
 ID 076039 standard; DNA; 5525 BP.
 AC 076039;
 DE 20-JUL-1995 (first entry).
 DR Retrovirus vector pPOL11-R2.
 KW Retrovirus; vector; pPOL11-R2; spleen necrosis virus; SNV;
 KW cytomagalovirus; CMV; intermediate-early promoter; IE promoter;
 KW long terminal repeat; LTR; encapsidation; gene transfer;
 OS Spleen necrosis virus.
 PN W09429437-A.
 PD 22-DEC-1994.
 PE 07-JUN-1994; U06415.
 PR 07-JUN-1993; US-073345.
 PA (UYNE-) UNIT NEW JERSEY.
 PI Dornburg RC:
 DR WPI: 95-036467/05.
 PT Recombinant retrovirus vector, contg. non-retroviral gene, - has
 PT ability to produce progeny virus, in helper cell which can infect
 PS host cell and form provirus
 Example: Page 14-16: 28pp: English.
 CC New recombination-free, highly efficient retroviral vectors
 CC pPOL11-R1 (given in 076038), pPOL11-R2 (076039) and pPOL11-R3
 CC (076040) were obtained by replacing the U3 region of the left
 CC LTR of spleen necrosis virus with the IE promoter/enhancer of CMV,
 CC and extension of the encapsidation region. The vectors allow
 CC cell-type specific gene expression and eliminate risks of
 CC downstream activation of cellular proto-oncogenes.
 SQ Sequence 5525 BP; 1264 A; 1422 C; 1457 G; 1382 T;

Query Match Best Local Similarity 76.0%; Score 238.6; DB 1; Length 5525;
 Matches 208; Conservative 86; Mismatches 14; Indels 17; Gaps 3;

OY 1 gnuaccucgagggguuugggaggaucgga---guugcgggagcgucggcggaagcucca 57
 DB 962 GGTACCTCCGAGAGGTTTGGAGAGATCGAGTGTGGCGGAGCTCCGAGAGCTCCA 1021
 OY 58 ccucgcgucagagggagggagcccgucgagcuc-----uguggaucugau 105

Mouse SRY-related gene.

FT		4307.	.4429
exon			

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FT exon 4707.4904
FT exon /*tag- g
FT exon 6193.6323
FT exon /*tag- h
FT exon 6501.6608
FT exon /*tag- i
FT exon 6751.6868
FT exon /*tag- j
FT exon 8335.8521
FT exon /*tag- k
FT exon 8719.8922
FT exon /*tag- l
FT exon 10124.10321
FT exon /*tag- m
FT exon 10650.11490
FT exon /*tag- n
FT 3'utr 11491.11531
FT /*tag- o
PN W09325669-A.
PD 23-DEC-1993.
PF 09-JUN-1993. SE0515.
PR 11-JUN-1993. SE-001809.
PR 12-JUN-1993. SE-001826.
PR 03-JUL-1993. SE-002088.
PR 19-MAR-1993. SE-000902.
PA (ASTRA) ASTRA AB.
PI Bjursell KG, Carlsson PNI, Enerback CSM, Hansson SL;
PI Linderberg UPP, Nilsson JA, Tornell JBF, Toernell JBF;
PI Enerback CSM;
DR WPI: 94-007527/01.
DR P-PSDB: R45189.
PT DNA encoding bile salt-stimulated lipase/carboxyl ester lipase -
PT expressed by transgenic non-human mammals and used as human milk
PT substitute, contains intron sequences
PS Claim 1, Page 43-51; 76pp. English.
CC The primers (Q54223-28) are used to amplify fragments of the
CC BSL / CEL gene, (Q54222). Which encodes a bile salt-stimulated
CC lipase / carboxyl ester lipase which when expressed by transgenic
CC animals can be used as a human milk substitute. The BSL is designed
CC to pass through the stomach and is activated in the small intestine.
CC As it has a broad substrate specificity it can mediate the complete
CC digestion of most dietary lipids.
SQ Sequence 11531 BP; 2464 A; 3527 C; 3280 G; 2260 T;

```

Query Match
Best Local Similarity 9.2%; Score 28.8; DB 1; Length 11531;
Matches 51; Conservative 24; Mismatches 77; Indels 0; Gaps 0;

```

QY 41 gcugccgggaagcucacccgcgcucagcagggagccgcucugagcucuguguanu 100
DB 7107 GCTCACTGCACCTCCACCTCTCGGCTCAAGTATCTCTCACTCACTCCATGTAG 7166
QY 101 cugauuguuugugacccgucuccaagagcgugauaauaagucuguguuuguguuug 160
DB 7167 CTGGGACTACAGCAGCATGCCCATGCCACAGATATTTTCTGTGTAGTAGGGAT 7226
QY 161 uuuguuaccuguguuugucgucacuuugcg 192
DB 7227 GGAGTTTCACTGCTTACTAGATGATCTCG 7258

```

RESULT 15
X32297

ID X32297 standard; DNA; 4795 BP.
AC X32297;
DT 22-JUN-1999 (first entry)
DE M. grisea PTH12 gene sequence.
KW Fungal pathogenicity; imidazole glycerol phosphate dehydratase; PTH2;
KW carnitine acetyl transferase; membrane associated pathogenicity protein;
OS homeodomain transcription factor; PTH3; PTH11; PTH12; ss.
PN M09913094-A2.

```

PD 18-MAR-1999.
PF 08-SEP-1998. U18730.
PR 10-SEP-1997; US-058460.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Svelgaard JA;
DR WPI: 99-1229247/19.
DR P-PSDB: Y06786.
PT New isolated fungal pathogenicity genes
PS Claim 33; Page 47-49; 50pp. English.
CC The invention relates to new isolated fungal pathogenicity genes,
CC designated PTH2, PTH3, PTH11 and PTH12 that are obtained from Magnaparcha
CC grisea. These novel genes encode proteins (Y06783-86) that are highly
CC homologous to the fungal carnitine acetyl transferase enzyme, fungal
CC imidazole glycerol phosphate dehydratase enzyme, fungal membrane
CC associated pathogenicity protein or fungal homeodomain transcription
CC factor respectively. The novel genes are implicated in fungal
CC pathogenicity. Inhibition of any of the genes PTH2, PTH3, PTH11 and PTH12
CC results in the reduction or elimination of the pathogenic phenotype of
CC the fungus. The isolated genes are useful in the design of screens to
CC identify inhibitors of the fungal pathogenic gene products. The present
CC sequence represents the PTH12 gene sequence.
SQ Sequence 4795 BP; 1220 A; 1338 C; 1067 G; 1170 T;

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Query Match
Best Local Similarity 9.1%; Score 28.6; DB 1; Length 4795;
Matches 22; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

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QY 121 uccaagacggugauaauaagucguguuuguuuuuuuuuaccuuguuuuuu 180
DB 3828 TCAAAAGCGGTGAATGCCAAGAGGCTGTGCGATTTTCTTTTGTGTGTATG 3887
QY 181 cguacac 187
DB 3888 TGTCTCT 3894

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Search completed: August 7, 2000, 09:21:37
Job time: 470 sec

Tue Aug 8 08:33:21 2000

us-09-214-124-2_copy_265_578.rng

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 11:56:12 ; Search time 3871.63 Seconds
(without alignments)
144.654 Million cell updates/sec

Title: US-09-214-124-2_COPY_452_578
Perfect score: 127
Sequence: 1 ugucgacagcgcccgcgaa.....ccucucgcgcgggauggg 127

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: em_est1: *
2: em_est2: *
3: em_est3: *
4: em_est4: *
5: em_est5: *
6: em_est6: *
7: em_est7: *
8: em_est8: *
9: em_est9: *
10: em_est10: *
11: em_est11: *
12: em_est12: *
13: em_est13: *
14: em_est14: *
15: em_est15: *
16: em_est16: *
17: em_est17: *
18: em_est18: *
19: em_est19: *
20: gb_est1: *
21: gb_est2: *
22: gb_est3: *
23: gb_est4: *
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25: gb_est6: *
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94: gb_gss2: *
95: gb_gss3: *
96: gb_gss4: *
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105: gb_gss9: *
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110: em_gss9: *
111: em_gss10: *
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114: gb_gss11: *
115: em_gss12: *
116: gb_gss12: *

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	Best Local Similarity	37.18;	Pred. No 17;		
	Matches 23; Conservative	19;	Mismatches	20;	Indels 0;
					Gaps
0y	51	uaanacuuugagagacuuuugcuccacaguuucgucuuugacuuugacuuugacuuucucc	110		
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Query Match	23.5%	Score 29.8:	DB 104:	Length 487:
Best Local Similarity	42.5%	Pred. No. 20:		
Matches 31:	Conservative 15:	Mismatches 27:	Indels 0:	Gaps 0
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DB	355	TTGTATTATCAACGCCCGAGGTTGTGCAATAGTGGAGAGTGTGTCTCTCCAGC	296	
OY	81	gucucucgucagu 93		

Transley, S. D.: Generation of ESTs from tomato root tissue unpublished (1999)
On Jul 7, 1999 this sequence version replaced
Contact: David Fritsch
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA

JOURNAL
MEDLINE
12140200
Nature 3/1 (634, Suppl.), 22-23
Other ESRs: THC171424
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA

```

/organism="Homo sapiens"
/db_xref="CBR:3847685
/db_xref="taxon:9606"
/clone IMAGE:219692"
/clone_1lb="Soares retina N2b4HR"
/sex="male"
/lssue_type="retina"
/dev_stage="55 year old"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ eye: Vector: pTPTD (Pharmacia) with a
modified polylinker: Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I...oligo(dT) primer (5'
TGTCACCATCTGACGAGGAGGAGGCGCCCTTTTCTTTTCTTTTCTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6

```


Tue Aug 8 08:33:23 2000

us-09-214-124-2_copy_452_578.rst

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Oy 100 ccuccucuccuccgcgc 118
Db 1670 CCACCTGCTTAATCCTGC 1688

RESULT 9

US-08-480-150A-9
; Sequence 9, Application US/08480150A
; Patent No. 5989550
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immuncontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,150A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/149,223
; FILING DATE: 09-NOV-1993
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Canis familiaris
; DEVELOPMENTAL STAGE: Juvenile
; HAPLOTYPE: Diploidy
; TISSUE TYPE: Ovary
; CELL TYPE: oocyte
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 206..2353
; US-08-480-150A-9

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Best Local Similarity 39.2%; Pred. No. 2.8;
Matches 31; Conservative 15; Mismatches 33; Indels 0; Gaps 0;

Oy 40 cggcungcgaaauacuuugggagucuuugcuccagugucgguuugacugcu 99
Db 1610 CTGCTGATTAATACCAATGTCACAAAGTCCTCTCCGTCGCTCACTGAGGCTGCT 1669
Oy 100 ccuccucuccuccgcgc 118
Db 1670 CCACCTGCTTAATCCTGC 1688

RESULT 10

US-08-458-731-9
; Sequence 9, Application US/08458731
; Patent No. 6001599
; GENERAL INFORMATION:
; APPLICANT: Harris Ph.D., Jeffrey D.
; APPLICANT: Hsu, Kuang T.
; APPLICANT: Podolski, Joseph S.
; TITLE OF INVENTION: Materials and Methods for Immuncontraception
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,731
; FILING DATE: 09-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/012,990
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/973,341
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 31745
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6653
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Canis familiaris
; DEVELOPMENTAL STAGE: Juvenile
; HAPLOTYPE: Diploidy
; TISSUE TYPE: Ovary
; CELL TYPE: oocyte
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 206..2353
; US-08-458-731-9

Query Match 20.6%; Score 26.2; DB 5; Length 2381;
Best Local Similarity 39.2%; Pred. No. 2.8;
Matches 31; Conservative 15; Mismatches 33; Indels 0; Gaps 0;

RESULT 13

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US-08-486-382-4/c
; Sequence 4, Application US/08486382
; Patent No. 5866327
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B.
; TITLE OF INVENTION: Association of Kinesin with Sensitivity
; TITLE OF INVENTION: To Chemotherapeutic Drugs
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 75 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,382
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/177,571
; FILING DATE: 05 JAN 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5866327nan, Kevin E.
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 93,354-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/715-1000
; TELEFAX: 312/715-1234
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2389 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
US-08-486-382-4

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RESULT 14
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; Sequence 4, Application US/09235546
; Patent No. 6043340
; GENERAL INFORMATION:
; APPLICANT: Gudkov, Andrei
; APPLICANT: Roninson, Igor B.
; TITLE OF INVENTION: Association of Kinesin with Sensitivity
; TITLE OF INVENTION: To Chemotherapeutic Drugs
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff, Ltd.
; STREET: 75 State Street
; CITY: Boston
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STATE: Massachusetts
COUNTRY.: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,382
FILING DATE:
APPLICATION NUMBER: US 08/177,571
FILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: No. 6043340man, Kevin E.
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-235-546-4

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Best Local Similarity 36.5%; Pred.No. 3.3;
Matches 27; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

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QY 110 cuucuccggcgaggga 123
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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RESULT 15
US-08-929-208-18/c
Sequence 18 Application US/08929208
Patent No. 6080244
GENERAL INFORMATION:
APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Genes And Genetic Elements Associated
TITLE OF INVENTION: With Sensitivity To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 75 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,208
FILING DATE:

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 11:56:08 ; Search time 3871.63 Seconds
(without alignments)
357.649 Million cell updates/sec

Title: US-09-214-124-2_COPY_265_578
Perfect score: 314
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5247842 seqs, 2204914090 residues

Total number of hits satisfying chosen parameters: 10495684

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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113: gb_est65:*
114: gb_est66:*
115: em_est49:*
116: gb_est67:*

	COMMENT
determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org . The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .	
FEATURES	
source	Location/Qualifiers 1..937 /organism="Drosophila melanogaster" /db_xref="taxon:7227" /clone_lib="RPCL-98" /clone="BACR14B21" /note="end : TER3"
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Best Local Similarity	13.6%; Pred. No. 6.2; 141; Indels 0; Gaps 0;
Matches	41; Conservative 119; Mismatches
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Db	KSTKMKSCBIBGKGGSGBSTGTCTGCCBCBKCBGYGBCCCYSTTCGCYTATC 653
OY	ccgcucagcagggagagcccucgaucagcagcucugugguauaucugaugugagaccguc 120
Db	KSCKCKGKTCTCGGCTTYKCGCGTGSBGYGSTSKCGIKTTYYTKETATTTTTTC 713
OY	121 uccaacagcguganaaunaagucguguuuguuuguuuuuuuacucugucuguuuguu 180
Db	TCTYBCGCKTTGCKTCTGYTTCTCTYTKCAYSYTYTSTSTCCGKKTKGTATGT 773
OY	181 cguaucugucagcagcgccucgcaauugugugccacacgcgcggcuugcgaaaua 240
Db	GCTCTSKTKKXTSSTKKCSCGSGCCCTCSYTGIGTCGSGSYSBVOSVCCTGCT 833
OY	241 uaauuuggaagacuuuugcucacagucuuucgquuuuguaucugucucuccucu 300
Db	CTSTGCSBCKGTCCTKCTBCKBSGKGSCGCTGCTSBSTKYCTCTTTCTGTIT 893
OY	301 c 301
Db	894 b 894
RESULT 11	
CNSU010E1	1101 bp DNA GSS 26-JUL-1999
LOCUS	Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION	BACN03K12 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL098851
VERSION	GI:5610462
KEYWORDS	GSS:
SOURCE	fruit fly
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage

	Query Match	Similarity	10.7%	Score	33.6;	D _B	64;	Length	284;
	Best Local	Conservative	31.2%;	Pred.	No. 11;	Mismatches	89;	Gaps	0;
	Matches	55;							
QY	26 ucgaagugggcgacgcgucgccgaaagccaccucccgcaccaaggagcaccccugauc	85							
	: : : : : : : : : : : : : : :								
Db	178 tttggagggggggccccccggggggggccccccccccccccgggggggggttga	119							

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	Best Local Similarity	28.0%	Pred. No. 13;		
	Matches	21;	Conservative	28;	Mismatches
				26;	Indels
					Gaps
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Db	257	TTCGTTTCGTTATAT	271		

Search completed: August 7, 2000, 11:56:12
Job time: 9746 sec

Thu Aug 8 08:33:21 2000

us-09-214-124-2_copy_265_578.rst

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Run On: August 7, 2000, 10:55:16 ; Search time 4994.97 Seconds
(without alignment)

263.781 Million cell updates/sec

Title:	US-09-214-124-2_COPY_452_578
Perfect score:	127
Sequence:	1 uugcgacacgcgcgcucgaa

Scoring table: IDENTITY_NUC

Searched: 972840 seqs, 5187315402 residues

Total number of hits satisfying chosen parameters: 1945680

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Minimum DB seq length: 0
Maximum DB seq length: 1000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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	10:	gb_pv2.*
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80:	gb_hic31*
81:	gb_vil1*
82:	gb_vil2*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match Length	DB	ID	Description
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2	127	100.0	5	5	A83548
3	125.4	98.7	4292	82	A83548 Sequence 1
4	120.6	95.0	1530	81	AF006605 Fowlpox
5	32	25.2	172078	40	RESNYX
6	32	25.2	187155	32	AL160276 Spleen necr
7	31.2	24.6	15089	4	AL160271 Homo sapi
8	30.2	23.8	3176	3	GGRRY3
9	30.2	23.8	27067	43	AF096675
10	30.2	23.8	165821	44	AC020041 Drosophi
11	30.2	23.8	226318	34	AC022005 Homo sapi
12	30	23.6	33556	43	AE003745 Drosophi
13	30	23.6	210788	11	AC020474 Drosophi
14	30	23.6	302815	34	CNS01D7 Drosophi
15	29.8	23.5	109616	8	AE003489 Homo sapi
16	29.8	23.5	126569	73	ATT10K17
17	29.8	23.5	214311	45	AC008420 Arabidops
18	29.6	23.3	63377	42	AC008834 Homo sapi
19	29.6	23.3	103150	65	AC018426 Homo sapi
20	29.4	23.1	37243	33	AC008720 Homo sapi
21	29.2	23.0	538	3	LMF8E5
22	29.2	23.0	2156	5	BOVSSMI
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Best Local Similarity 70.9%; Pred. No. 7.5e-29;
Matches 90; Conservative 36; Mismatches 1; Indels 0; Gaps 0;
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Db 1690 TGTGACAGCCGCTGCAATGGTGTACCCACACCGCGCGGTGCAATATACCTTG 1749
OY 61 gagagcucucucgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 120
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OY 121 ggauggg 127
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Db 1810 GGATGG 1816

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REFERENCE
AUTHORS 1 (bases 2 to 470)
TITLE Shmotohno,K., Mizutani,S. and Temin,H.M.
JOURNAL Sequence of retrovirus provirus resembles that of bacterial
MEDLINE Nature-285 (5766), 550-554 (1980)
80254544
REFERENCE 2 (bases-1 to 1530)
AUTHORS Q. Rear,J.J. and Temin,H.M.
TITLE Spontaneous changes in nucleotide sequence in proviruses of spleen
JOURNAL necrosis virus,-an avian retrovirus
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 79 (4), 1230-1234 (1982)
82174569
COMMENT The meaning of the substitution at 739-749 is not completely clear
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Best Local Similarity 37.58; Pred. No. 5.4;
Matches 33; Conservative 20; Mismatches 35; Indels 0; Gaps 0;

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Db 156440 CTCACCGCGGCTCATATGCTCTGCTCAATGATGAGACTGATTTGCCCTAAATGTGTCTCC 156381
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QY      89 uuuugacucgucucucucucucucg 116
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Db 156380 TTCTCTGCTGCGCTGCGCTGCTCTG 156353

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RESULT 6
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DEFINITION Homo sapiens chromosome 9 clone RP11-323H21 map g34.1-34.3, ***
ACCESSION AL160271
VERSION    AL160271.1 GI:7242465
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 187155)
AUTHORS    Plumb, B.
TITLE      Direct Submissio
JOURNAL    Submitted (11-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humuqery@sanger.ac.uk Clone
            requests: clonerequests@sanger.ac.uk
            IMPOREANT: This sequence is unfinished and does not necessarily
            represent the correct sequence. Work on the sequence is in
            progress and the release of this data is based on the understanding
            be contaminated with foreign sequence from E.coli, yeast, vector,
            segments. Contig_ID: 00010 Length: 5345bp

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Contig_ID: 00088 Length: 1172bp
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Contig_ID: 00129 Length: 2048bp
Contig_ID: 00139 Length: 3817bp
Contig_ID: 00190 Length: 3761bp
Contig_ID: 00197 Length: 1526bp
Contig_ID: 00217 Length: 2123bp
Contig_ID: 00239 Length: 3564bp
Contig_ID: 00249 Length: 1983bp
Contig_ID: 00250 Length: 1222bp
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Contig_ID: 00346 Length: 2165bp
Contig_ID: 00350 Length: 6078bp
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Contig_ID: 00418 Length: 1122bp
Contig_ID: 00428 Length: 1849bp
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Contig_ID: 00454 Length: 1724bp
Contig_ID: 00488 Length: 1163bp
Contig_ID: 00510 Length: 9723bp
Contig_ID: 00510 Length: 2269bp
Contig_ID: 00534 Length: 4912bp
Contig_ID: 00545 Length: 1471bp
Contig_ID: 00555 Length: 2813bp
Contig_ID: 00584 Length: 1135bp
Contig_ID: 00591 Length: 6713bp
Contig_ID: 00599 Length: 5629bp
Contig_ID: 00614 Length: 1899bp
Contig_ID: 00637 Length: 2121bp
Contig_ID: 00654 Length: 2610bp
Contig_ID: 00677 Length: 2010bp
Contig_ID: 00714 Length: 4541bp
Contig_ID: 00760 Length: 1208bp
Contig_ID: 00764 Length: 1312bp
Contig_ID: 00766 Length: 1016bp
Contig_ID: 00770 Length: 7390bp
Contig_ID: 00770 Length: 1974bp
* NOTE: This is a 'working draft' sequence. It currently
* consists of 46 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
5345: contig of 5345 bp in length
5346 6145: gap of 800 bp
6146 7474: contig of 1329 bp in length
7475 8274: gap of 800 bp
8275 9446: contig of 1172 bp in length
9447 10246: gap of 800 bp
10247 12283: contig of 2037 bp in length
12284 13083: gap of 800 bp
13084 18993: contig of 5916 bp in length
18994 19799: gap of 800 bp
19800 21847: contig of 2048 bp in length
21848 22647: gap of 800 bp
22648 26464: contig of 3817 bp in length
26465 27264: gap of 800 bp
27265 31025: contig of 3761 bp in length
31026 31825: gap of 800 bp
31826 33351: contig of 1526 bp in length
33352 34151: gap of 800 bp
34152 36274: contig of 2123 bp in length
36275 37074: gap of 800 bp

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Db  38229 CTCACCTGCAGCANCATATTGCTGTGACTAATTGGAGAGATTTCCTTAATAATGTGTCTCG 38170
QY    89  uuuguacucguccucucucucucucucucg 116
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Db  38169 TTCCTCTTGCCTGCCCTCCCTGCTCTCTG 38142

RESULT 7
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LOCUS      G.gallus mRNA for ryanodine receptor type 3.
DEFINITION
ACCESSION  X95267
VERSION    X95267.1 GI:1212911
KEYWORDS   ryanodine receptor 3; RYR3 gene.
SOURCE     chicken.
ORGANISM   Gallus gallus
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            Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE  1 (bases 1 to 15089)
AUTHORS   Ottini,L., Marzital,G., Conti,A., Charlesworth,A. and Sorrentino,V.
TITLE     Alpha and beta isoforms of ryanodine receptor from chicken skeletal
         muscle are the homologues of mammalian RyR1 and RyR3
JOURNAL    Biochem. J. 315 (Pt 1), 207-216 (1996)
MEDLINE    96207583
REFERENCE  2 (bases 1 to 15089)
AUTHORS   Sorrentino/V.
TITLE     Direct Submission
JOURNAL    Submitted (18-JAN-1996) V. Sorrentino, DIBIT, San Raffaele
           Scientific Inst., via Olgettina 58, I-20132, Milano, ITALY
FEATURES
source
gene
CDs

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RESULT 12

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RESULT 13
CNS01D7/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
SOURCE

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Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-1070N10
of RPCL-11 library from chromosome 14 of Homo sapiens (Human),
complete sequence.
AL133467
AL133467.2 GI:7406475
HTG: HTGS_DRAFT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 210788)
Genoscope.
Direct Submission
Submitted (31-MAR-2000) to the EMBL/Genbank/DBJ databases
On Apr 3, 2000 this sequence is unfinished and does not necessarily
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
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Location/Qualifiers
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George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Blazell, M.D., Zhang, Q., Chen, L.X., Brindon, R.C., Rogers, Y.H., Blazell, M.D., Zhang, Q., Chen, L.X., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Champe, M., Pfeiffer, B.D., Milos, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Plamkovich, C., Baldwin, D., Ballew, R.M., Basu, A., Batendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brocktein, P., Brottier, P., Butts, K.C., Busam, D.A., Butler, H., Cadieu, E., Center, A., Cherry, J.M., Chery, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablo, B., Delcher, A., Deng, Z., Dones, M., Dugan-Rocha, S., Dunkov, B.C., Dodson, C., Doup, L.E., Downes, M., Evansangelista, C.C., Ferrez, C., Fleischmann, W., Foster, C., Gabriellian, A.E., Gar, N.S., Galtberg, M.W., Glasser, K., Glodde, A., Gong, F., Gorrell, J.H., Gu, E., Guan, P., Harris, M., Harris, N.L., Harvey, D., Helman, T.O., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Koditz, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lascko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, X., Lin, X., Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Misha, N.V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Nusskern, D.R., Pacle, J.M., Palazcolo, M., Plutan, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reiter, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shier, B.C., Siden-Klamos, I., Simpfendorfer, S., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stampleton, M., Strong, R., Sun, E., Svrtk, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zhong, J.S., Zhong, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X.H., Zeng, F.N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M., and Venter, J.C., The genome sequence of *Drosophila melanogaster* Science 287 (5461), 2185-2195 (2000)

2 (bases 1 to 302915)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA

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TITLE Direct Submission
JOURNAL Submitted (19-JAN-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: blochem@mps.biochem.mpg.de, mayer@mips.biochem.mpg.de, Project Coordinator: Marcel Salanoubat and Francis Queller, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE, 2 rue Gaston Cremieux, BP191, 91006 Evry Cedex, France;
http://www.genoscope.cns.fr
COMMENT Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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ENAIJPCPNONRNKRKDEKFKKSGSTRKNKSSSENEKLPYHVARQGAATSHSLA
ERARERKIMARKLOELVEPCDKIGGTALVLDIINHVSLOGROVEMLSRLAAVAP
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GKRYTDTDSIIAHGCLSLGKLAGEKMRDLADELTPVADDEFIQRORFEMVEGD
EDTVYRQIRDPHVGGEPELFMAHVLOMPPTVYMKDKKAGGLSIADYQOEYKDDP
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13360.. 13903
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RIBOSOMAL PROTEIN L21 - Arabidopsis thaliana,
SWISSPROT: R21_ ARATH"
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complement(13360.. 13528)
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FAGNSLCEPFLQCKDEGTNPKLVAPREGSOTILPKPNPSFIDKGRKNKPTGS
MDEGFLELEDLLRASAVYVGRSGCIYRVVAGKSTVATFTSIVAVVRISDG
DATWRKDENEVEAISRYOHNPVYLAEDERLLTIDYIRNGSLVSLAGGPS
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TSLVSGYSLKISLSATRSQSDQTYLTGATVTRTAPVAVLAPEARASSGCLTSOK
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19544..19685

Intron

Query Match      23.5%; Score 29.8; DB 8; Length 109016;
Best Local Similarity 31.5%; Pred. No. 27;
Matches 23; Conservative 23; Mismatches 27; Indels 0; Gaps 0;

QY 43 cuugcgaaunaacuuugagagucuuuugccuccagucuuucguuugacuucgu 102
|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 41692 CTTCTTAAATACTTATGATCTTTCTTTTAAAGCAATGAGATTGTCTCTCT 41751

QY 103 ccucuccucuc 115
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 41752 TCTCACCATATCC 41764

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Search completed: August 7, 2000, 10:56:58
Job time: 6192 sec

Query Match	100.0%;	Score 127;	DB 1;	Length 940;
Best Local Similarity	100.0%;	Pred. No. 2,7e-33;		
Matches 127, Conservative	0;	Mismatches	0;	Gaps 0

Db 934 GGAUGGG 940

33

Query Match	98.7%;	Score 125.4;	DB 1;	Length 4643;
Best Local Similarity	70.9%;	Pred. No. 1.5e-32;		
Matches	90;	Conservative	36;	Mismatches 1;
				Indels 0;
				Gaps 0;

Db 2161 GGATGGG 2167

50

M

Db 1276 GGA 1278

Query Match	91.8%;	Score 116.6;	DB 1;	Length 5525;
Best Local Similarity	69.9%;	Pred. No. 1,3e-29;		
Matches	86;	Conservative	33;	Mismatches 4;
				Indels 0;
				Gaps 0;

RESULT	6
Q76038	standard; DNA; 5528 BP.

pPOLL1-R1 (given in Q76038), pPOLL1-R2 (Q76039) and pPOLL1-R3

Query Match	91.8%	Score 116.6	DB 1	Length 5528
Best Local Similarity	69.9%			
Matches	86	Pred. No. 1.3e-29		

RESULT	7
Q76041	
ID	Q76041 standard; DNA; 3878 BP.
CC	Q76041.

Query Match	89.4%	Score 113.6	DB 1	Length 3878
Best Local Similarity	69.2%	Pred NO. 1.1e-28		
Matches	83	Conservative	33	Mismatches 4
			Indels	0
			Gaps	0

Q80523 standard; DNA; 3946 BP.
Q80523;

15-JUL-1995 (first entry)
Human mcl-1 gene,
Myeloid cell leukemia-associated gene; mcl-1; diagnostic.


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Query Match      21.33; Score 27; DB 1; Length 49998;
Best Local Similarity 34.78; Prid. No. 12;
Matches 26; Conservative 19; Mismatches 30; Indels 0; Gaps
QY 45 ugcgaanaaacuuuugggagagcuuuuugccuacgagucucuccgmuuuuagacugcucc 104
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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[illegible]

Tue Aug 8 08:33:22 2000

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Page 6

Db 961 TTCTGCCCTTTCAGCCTCTCAAGCCACATCTTGCGCTGCAGTA 1010

RESULT 14

ID 081700 standard; cDNA to mRNA; 1335 BP.
AC 081700;
DT 15-MAR-1995 (first entry)
DE C2P2(75-520).
KW Canine; dog; zona pellucida; ZP; C2P2; contraceptive; vaccine;
KW antigen; ss.
OS Canis familiaris.
PN J06189766-A.
PD 12-JUL-1994.
PF 25-DEC-1992; 359265.
PR 25-DEC-1992; JP-359265.
PA (TOFU) TONEN CORP.
PI: 94-259553/32.
DR New DNA sequence encoding canine zona pellucida C2P2 - useful for
PT the prodn. of a canine contraceptive vaccine antigen
PS Disclosure: Page 4-5; 10pp; Japanese.
CC The C2P2 DNA (070072) was prepd. by the cloning of C2P2(75-520) -
CC 081700 using the primers given in 070073-74, C2P2(1-65) - Q81804
CC using the primers given in 070082-83, C2P2(42-103) - Q81803 using
CC the primers given in 070079-81 and C2P2(487-713) - Q81957 using the
CC primers given in 070075-78.
SQ Sequence 1335 BP; 385 A; 331 C; 277 G; 342 T;

Query Match

Best Local Similarity 20.6%; Score 26.2; DB 1; Length 1335;
Best Local Similarity 39.2%; Pred. No. 8.1; Mismatches 33; Indels 0; Gaps 0;
Matches 31; Conservative 15;

QY 40 cggcugcgaaauaacuungagagucuuuugccuacagucuuucguuugacu 99

Db 1174 CTGCTGATTAATACCAATGTCCTTCCTCCCGGCGCTCAGTAGGCTGTGT 1233

QY 100 ccucucucucucucgcgc 118

Db 1234 CCACTTGCCCTTAATCCTGC 1252

RESULT 15

ID 070072 standard; cDNA to mRNA; 2216 BP.

AC 070072;
DT 15-MAR-1995 (first entry)

DE Canine zona pellucida C2P2.

KW Canine; dog; zona pellucida; ZP; C2P2; contraceptive; vaccine;
KW antigen; ss.

OS Canis familiaris.

PN Key

FT cds Location/Qualifiers
FT 46..2187
FT /*tag= a

PN J06189766-A.

PD 12-JUL-1994.

PF 25-DEC-1992; 359265.

PR 25-DEC-1992; JP-359265.

PA (TOFU) TONEN CORP.

PI: 94-259553/32.

DR P-PSDB; R60101.

PT New DNA sequence encoding canine zona pellucida C2P2 - useful for
PS the prodn. of a canine contraceptive vaccine antigen

CC Claim 1: Page 8-10; 10pp; Japanese.

CC 081700 using the primers given in 070073-74, C2P2(1-65) - Q81804
CC using the primers given in 070082-83, C2P2(42-103) - Q81803 using
CC the primers given in 070079-81 and C2P2(487-713) - Q81957 using the
CC primers given in 070075-78.

SO Sequence 2216 BP; 606 A; 549 C; 487 G; 574 T;

Best Local Similarity 39.2%; Pred. No. 9.4;
Matches 31; Conservative 15; Mismatches 33; Indels 0; Gaps 0;

QY 40 cggcugcgaaauaacuungagagucuuuugccuacagucuuucguuugacu 99

Db 1444 CTGCTGATTAATACCAATGTCCTTCCTCCCGGCGCTCAGTAGGCTGTGT 1503

QY 100 ccucucucucucucgcgc 118

Db 1504 CCACTTGCCCTTAATCCTGC 1522

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Job time: 478 sec

Query Match

20.6%; Score 26.2; DB 1; Length 2216;

Tue Aug 8 08:33:22 2000

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